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AAVESAS represent the EST-related proteins. AAVESAS to AAVESAS to AAVESAS a sequences, corresponding to human secreted proteins. AAVESAS to AAVESAS and be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated to regions (UTRs) and upstream regulatory regions which control the conton of the world many. The ESTS are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTS can also be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals, or in diagnostic procedures to identify individuals, or in diagnostic procedures to identify individuals, or the caulting from abnormal gene expression. The products may also be used in gene expression or a popphedia can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a call. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have the call and the identification of new secreted proteins is valuable. AAZ42249 to AAZ42244 and AAVE4644 to AAVE4560 represent:
                                                                                                                                                                                                                                                                                                            sequences used in the exemplification of the present invention
                                           to AAZ43075 represent novel 5'
                 Page 605-606; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, 5' EST; expressed sequence tag; secreted protein; diagnosis;
gene therapy; chromosome mapping; upstream regulatory sequence;
forensic; location; development; protein synthesis; stability;
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 Mismatches:
Indels:
                                                      US-08-728-463B-205 (1-403) x AAR41285 (1-142)
                               Gaps:
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 77.46%
76.04%
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N-PSDB; AAZ42290.
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Local Similarity:
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28-APR-1998;
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                                                                                                                                                                                                                                                                                                                  21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSer***ThrLeuSerLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GlyLysGlyLeuGluTrpIleGlyTyrIleTyrTyrSerGlySerThrAsnTyrAsnPro
                                                                                                                                                                                                                                        1 Met***HisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln
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                                           Conservative:
Mismatches:
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Matches:
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                    564.50
82.86%
79.29%
75.98%
                                           Percent Similarity:
Best Local Similarity:
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Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS; CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light; chain; epitope; immune deficiency.
298 AAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGAGTAATT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA from the known hybridoma F105 was converted to cDNA and this subjected to PCR amplification using primers corresp. to appropriate parts of the heavy or light chains and having restriction sites to permit cloning. The extension prods. were isolated and sequenced. The recombinant human monoclonal antibody (MAb) binds to a discontinuous epitope on the HIV gpl20 envelope glycoprotein, blocks the binding of gpl20 to the CD4 receptor, and neutralises a broad range of HIV isolates. The MAb may be used to treat immune deficiency, esp. at doses of 0.1-10 mg/kg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA segments encoding monoclonal antibody - which binds to gp120 and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV infection
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(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                       F105 rearranged variable region heavy chain.
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/label= mat_protein
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121 ValSerSer 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in new-born rhesus positive babies. Recombinant IgM-D7C2 can be produced by insect cells which have been transformed by a baculoviral vector comprising a D7C2 expression cassette. The present sequence is that of the variable region of the IgM-D7C2 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing
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/label= CDR2
/note= "complementarity determining region"
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                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haemolysis in new-born babies
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(PROT-) PROTEINE PERFORMANCE.
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 Homo sapiens
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the antibodies and fragments of the antibodies described in the method
                                                                                                                                      21 ThrCygAlaValTyrGlyGlyGerPheSerGlyTyrTyrTrpSerTrplleArgGlnPro
                                                                                                                                                                           118 ACCIGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCC
                                                                                                                                                                                                               CCAGGTAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTACAAC
                                                                                                                                                                                                                          CCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune system associated protein; HISAP-4; immune disorder;
infection; autoimmune disease; cancer.
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112
112
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                                                        Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                         AAB36206 standard; protein; 473
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                                                      1.37e-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Yue H, Lal P,
Hillman JL, Au-Young J;
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N-PSDB; AAC66522.
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Best Local Similarity:
Query Match:
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          of the invention.
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                                             Alignment Scores:
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The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISAPs). These can be used in the diagnosis and treatment of various autochmune disorders, infections and cell proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, osteoarthritis, rheumatcid arthritis, scleroderma, systemic lupus erythematosus, arteriosclerosis, cirrhosis and cancer.
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                 New human immune system associated proteins (HISAP) and polynucleotides encoding the HISAP, useful for diagnosing, treating or preventing immune or cell proliferative disorders or infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humah monoclonal antibody; immunoglobulin isotype IgM; agglutination; rhesus positive; rhesus negative; haemolysis; heavy chain; variable region; insect host cell; baculovirus; recombinant production.
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                                                                       Claim 1; Column 53-56; 54pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a human monoclonal antibody to parathyroid hormone related protein (PTHrP). The monoclonal antibody or lits fragments. following the stimulation of PTHrP has the following properties: (a) inhibits intracellular elevation of CAMP; (b) inhibits the release of calcium from bone; or (c) inhibits elevation of blood calcium content. The monoclonal antibody can be used in the treatment of hypercalcaemia, rheumatoid arthritis, cancer of bone including metastasis, pain, fracture, cachexia, diseases of teeth, periodontal diseases and gingiva, sepsis, systemic inflammatory response syndrome (SIRS) and hypohosphatemia. It has antiarthritic, cytostatic and antiinflammatory activities. The present sequence represents a human PHTHP monoclonal antibody clone protein sequence from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human monoclonal antibody to parathyroid hormone related protein. -
                            Human, parathyroid hormone related protein, PTHrP; monoclonal antibody; hypercalcaemia; rheumatoid arthritis, bone cancer; metastasis; pain; fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis; systemic inflammatory response syndrome; SIRS; hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
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including metastasis, and pain
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N-PSDB; AAA13938.
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26-JUN-1998;
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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulati; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                             101 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaSerAlaValThrTyr 120
                                                                                                      TCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCCCTGAAG 300
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17-CCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-273739P.
25-MAY-2001; 2001US-293499P.
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and/or remedies for platelet reduction-associated blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia. The antibody can act as a TPO signal transduction agonist by transducing a signal into cells by crosslinking a TPO receptor to exert TPO agonism. This is the amino acid sequence of a thrombopoietin (TPO) agonism antibody associated protein.
                                                                                                                                                                      GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC
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TPO receptor; platelet reduction-associated blood disease;
thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction.
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2001WO-JP03288.
2001JP-0277314.
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Best Local Similarity:
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17-APR-2001; 2
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                                                                                                                                                                                                                                                                                          The invention describes a modified antibody comprising at least 2 heavy chain variable domains and 2 or more light chain variable domains of an antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing the TPO receptor to crosslink. The antibodies are useful in preventives and/or remedies for platelet reduction-associated blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia. The antibody can act as a TPO signal transduction agonist by transducing a signal into cells by crosslinking a TPO receptor to exert TPO agonism. This is the amino acid sequence of a thrombopoietin (TPO) agonist antibody associated protein.
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                                                                                                                      Degraded thrombopoietin agonist antibodies containing H and L chain V domains of monoclonal antibody, useful in preventives and/or remedies for blood diseases, thrombocytopenia following cancer chemotherapy or
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  Tsunoda H,
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Tsuchiya M, Ohtomo T,
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The invention describes a modified antibody comprising at least 2 heavy chain variable domains and 2 or more light chain variable domains of an antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing the TPO receptor to crosslink. The antibodies are useful in preventives
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TPO receptor; platelet reduction-associated blood disease;
thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction.
                                        Degraded thrombopoietin agonist antibodies containing H and L chain V domains of monoclonal antibody, useful in preventives and/or remedies for blood diseases, thrombocytopenia following cancer chemotherapy or
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12-SEP-2001; 2001JP-0277314.
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                                                                        The invention describes a modified antibody comprising at least 2 heavy chain variable domains and 2 or more light chain variable domains of an antibody, and exhibite thrombopoietin (TPO) agonistic effect by causing the TPO receptor to crosslink. The antibodies are useful in preventives and/or remedies for platelet reduction-associated blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia. The antibody can act as a TPO signal transduction agonist by transducing a signal into cells by crosslinking a TPO receptor to exert TPO agonism. This is the amino acid sequence of a thrombopoietin (TPO) agonism antibody associated protein.
                                                                                                                                                                                                                                                                                                                                                                   Modified antibody; thrombopoietin; TPO; agonist;
TPO receptor; platelet reduction-associated blood disease;
thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction.
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                                                      GACACGCTGTGTATTACTGTGCGAGAGTAATT---
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17-APR-2001; 2001WO-JP03288.
12-SEP-2001; 2001JP-0277314.
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N-PSDB; ABK71396

leukaemia

WO200233072-A1.

Mus sp

25-APR-2002

30-JUL-2002

ABG35331;

RESULT

8 용 US-08-728-463B-205 (1-403) x ABG35331 (1-133)

Best Local Similarity:

Query, Match:

Percent Similarity:

Alignment Scores:

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133

Sequence

Location/Qualifiers

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Key
Peptide
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respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present salequence represents a human ovarian antigen of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                              120
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126 SerSerTrpTyrProArgAlaGluTyrPheGlnHisTrpGlyGlnGlyThrLeuValThr 145
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GCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTATGGTGGGTCC 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 AlaGiyLeuLeuLysProSerGluThrLeuSerLeuThrCysThrValTyrGlyGlySer 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 PheSerGlyTyrTyrTrpSerTrplleArgGlnProProGlyLygGlyLeuGluTrpIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGCAGCTACAGCAGTGGGGC
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                                                                                                                                          Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive calls but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in new-born rhesus sositive babies. Recombinant IgM-D7C2 can be produced by insect cells which have been transformed by a baculoviral vector comprising a D7C2 expression cassette. The present sequence is that of a recombinant IgM-D7C2 heavy chain fused downstream of a mouse VH signal peptide.
                                                                20.472
/labbl= heavy chain
/note= "human gamma 1 chain constant region
and the variable region from anti-rhesus
antibody D7C2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing
                                            peptide sequence
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115
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Mismatches:
Indels:
1..19
/label= signal_peptide
/note= "mouse VH signal per
synthetic linker"
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                        Chaabihi H, Edelman L, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 35-37; 46pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haemolysis in new-born babies
                                                                                                                                                                                                                                                                                                                                                (INSP ) INST PASTEUR.
(PROT-) PROTEINE PERFORMANCE.
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595.00
86.67%
85.19%
80.08%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                            FR2724182-A1
                                                                                                                                                                                                                                                                                                            02-SEP-1994;
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                                                                              Protein
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Human monoclonal antibody; immunoglobulin isotype IgM; agglutination; rhesus positive; rhesus negative; haemolysis; gamma 1 heavy chain; variable region; insect host cell; baculovirus; recombinant production.

Homo sapiens Synthetic.

Anti-rhegus D recombinant antibody D7C2 heavy chain.

30-OCT-1996

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AAR93166 standard; Protein; 472

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The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleorides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprishing human ovarian antigens to polynucleorides, antibodies against human ovarian antigens, and the use cc ovarian antigen polynucleorides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and cestating, prognosing or preventing various ovary and/or breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian oysts, and dysmenorrhoea), endocrine collections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, cophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders
                                                                        241 TCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCCCTGAAG 300
                                                                                                   Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gestrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostetic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                    301 CTGAGCTCTGTGACCGCCGCGCACACGCCTGTGTATTACTGTGCGAGA 348
                                                                                                                                                                                             101 LeuSerServalThrAlaAlaAspThrAlaValTyrTyrCysAlaArg 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ovarian antigen HVVDH44, SEQ ID NO:4331.
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                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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N-PSDB; ABQ56276.
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ABP43199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein sequences (AAR66295-51) are novel human immunoglobulin heavy
                                                                                                                                                                                           Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain; cosmid; placenta; vector; pJB81; E.coli; mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA fragment comprising human immunoglobulin Vh genes - for the production of human immunoglobulin in mammalian hosts
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Matches:
Conservative:
Mismatches:
                                                                                                                                              Human immunoglobulin variable heavy chain #30.
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    AAR66324 standard; Protein; 116 AA.
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100.00%
100.00%
83.71%
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                                                                                                 03-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Honjo T, Matsuda F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-006791/01.
N-PSDB; AAQ78972.
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                24-NOV-1994
                                                 AAR66324;
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30-MAR-2000; 2000WO-JP02022.
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gene, protein, its antibodies, agonists and antagonists are suitable for diagnosing and treating many diseases, including cancer, immune system disorders (such as inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative colitis), complications of cancer, haemodialysis and extracorporeal circulation, trauma and haematopoietic cancer (such as leukaemia) and infections caused by bacteria, viruses, fungi or parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                   345
                                                                                                                                                                                                                                                                                                                                                                                                                                                           384
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|ArgGlyArgSerAspSerSerGlySerProTyrGlyLeuAspTyrTrpGlyGlnGlyThr 147
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                                                                                                                                                                                                                                                                                            28 ValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeuThr
                                                                                                                                                                                                                                                                                                                        121 TGCGCTGTCTATGGTGGGTCCTTC------AGTGGTTACTACTGAGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunoglobulin heavy chain amino acid sequence.
                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                     US-08-728-463B-205 (1-403) x AAY96290 (1-537)
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650.00
88.36%
87.67%
87.48%
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                                                                                                                 537 AA;
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                                                                                                                                                                  Percent Similarity:
                                                                                                                                     Alignment Scores:
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                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                This invention relates to a method for the production of a monoclonal antibody. The antibody is produced by inserting a gene encoding an immunoglobulin heavy chain polypeptide into cells which produce a monoclonal antibody recognizing the immunoglobulin, and culturing the transformant to express the antibody. The invention also includes monoclonal antibody-expressing cells transformed by the method, and transgenic non-human animals containing the cells and expressing a human antibody. The method results in the enhanced expression of a monoclonal antibody. In the method results in the enhanced expression of a monoclonal antibody for diagnostic and therapeutic use. The present sequence represents a human immunoglobulin heavy chain amino acid sequence, the CDNA encoding the protein is used in an example of the method of the
                                                                                                                                                                                            Transformation of a hybridoma with a gene encoding an immunoglobulin
heavy chain polypeptide for enhanced production of monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 CysAlaValTyrGlyGlySerPheSerGlyTyrTyrTrpThrTrpIleArgGlnProPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GlyLysGlyLeuGluTrpIleGlyGluIeIleHisHisGlyAsnThrAsnTyrAsnPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 ValGInLeuGInGInTrpGlyAlaGlyLeuLeuLy8ProSerGluThrLeuSerLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCGCTGTCTATGGTGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCA
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                                                                                                                                                                                                                                                                                           Example 2; Page 40-43; 48pp; Japanese.
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93.38%
90.44%
86.94%
                                                                        Kusunoki C, Fukushima A;
(NISB ) JAPAN TOBACCO (ABGE-) ABGENIX INC.
                                                                                                                     WPI; 2000-611721/58.
N-PSDB; AAA09695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462 AA;
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Best Local Similarity:
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Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders
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                                                              ArgProHisArgTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer
                                               ------AATTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gorgone GA, Baughn MR;
                                                                                                                                                                                                                                                                   Human; immunoglobulin; IGFAM-2; IGFAM; immune disorder; cancer;
infection; inflammation; haematopoiesis; AIDS; allergy.
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Yang J;
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| /label= signal_peptide
| 27.537
| /label= IGFAM-2
| /label= | g_domain
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                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
                                                                                                                                         AAY96290 standard; protein; 537 AA
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label Ig domain
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| label = Ig_domain
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/label=_Ig_domain
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                                                                                                                                                                                                                                      Human IGFAM-2 immunoglobulin.
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98US-0113635.
99US-0128194.
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Lal P, Hillman JL,
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/label= Ic
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22-DEC-1998;
07-APR-1999;
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                                                                                                           RESULT
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                                                                           원
                                                                                                                                                                                                                                                                                                                                                        The present sequence is the heavy chain variable region of a human tumour-specific monoclonal antibody. Neoplastic cells selectively express antibodies which are not present on normal cells. Thus monoclonal antibodies can be produced that are specifically directed against tumour-specific antigens. The antibodies can be conjugated to cytotoxic or cytostatic agents and used to selectively target cancer cells for the elimination of tumours. They can also be linked to diagnostic moieties that allow the imaging of neoplastic cells. Nucleic acids encoding human tumour-specific monoclonal antibodies can be used to express the cantibodies with higher affinity or higher selectivity for tumour cells. Tumour-specific antibodies were produced by hybridomas that were generated by in vitro immunisation of human spleen cell cultures with becast carcinoma cells. The nucleic acid encoding the monoclonal antibody was then isolated from the hybridoma by RT-PCR. The present sequence was produced by LH11238 hybridoma cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                    New tumor-specific human monoclonal antibody, useful for the treatment and diagnosis of cancer, comprises at least one complementarity determining region -
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/label= LH11238_antibody_heavy_chain_variable_region
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94.24%
93.53%
91.59%
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N-PSDB; AAA52907.
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                       (IXSY-) IXSYS INC.
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                               WO200032635-A2
                                                                                         01-DEC-1999;
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1 ATGAAACACCTGTGGTTCTT.......CCTGGTCACCGTCTCCTCAG 403
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-LOOPEXT=0 - ONTITS=bits - START=1 - END=-1 - MARTRIX=blosum62 - TRANS=human40.cdi
-LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN-0 - ALIGN=15
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- NOTEM=12pc - NOTEM=10 - VARENDS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
- FGAFEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELEXT=7
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Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Human; LH11238 monoclonal antibody; hybridoma; tumour-specific; cancer; cytostatic; cytotoxic; heavy chain variable region.

Homo sapiens

Key Peptide Protein

Location/Qualifiers. 1..19 /label= Signal_peptide 20..139

Human LH11238 monoclonal antibody heavy chain variable region.

20-SEP-2000 (first entry)

AAY99556;

ALIGNMENTS

AAY99556 standard; Protein; 139 AA

AAY99556

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Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
Fara A. Cloned human immunoglobulin heavy chain gene with a novel directrepeat sequence in 5 flanking region.";
Fara A02101; GlHUH2.
FIRSP, PO1825; 7PAB.
InterPro; IPR003006; Ig_MHC.
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-DB=SwisSProt_40 -OFWT=fastan -SUFPIX=xFp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
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19 heavy chain V-II redion NEWN.
Endon eaplens (Human).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=78066916; PubMed=618887;
Saul F.A., Amzel L.M., Poljak R.J.;
"Preliminary refinement and structural analysis of the Fab fragn Transman immunoglobulin new at 2.0-A resolution.";
J. Biol. Chem. 253:585-597(1978).
--- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
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IMMUNOGLOBULIN V. region; 3D-structure.
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Poljak R.J., Nakashima Y., Chen B.L., Konigsberg I.
"Amino acid sequence of the VH region of a human immunoglobulin (IgG New) ",
Biochemistry 16:3412-3420(1977).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=82222235; PubMed=6806818;
Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.
"Complete amino acid sequence of the delta heavy chain of immunoglobulin D.";
Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854 (1982).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pheavy chain V-II region WAH.
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US-08-728-463B-205 (1-403) x HV2I_HUMAN (1-146)
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GlycoSuiteDB; P01824; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IRR003596; Ig_v.
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SMART; SN00406; IGv, 1.
Immunoglobulin V region.
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1 ATGAAACACCIGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
Jilka R.L., Pestka S.; "Amino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin heavy chain.";
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Mus.
NCBI_TaxID=10090;
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Rinfret A., Horne C., Dorrington K.J., Klein M.;
"Cloning, sequencing and expression of the rearranged MOPC 315 VH
                                                                                                                                                                                                                                                                                                                                                                                                          101 AlaGlyCysIleAspValTrpGlyGlnGlySerLeuValThrValSerSer 117
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Mismatches:
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01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Igh heavy chain V region MOPC 315 precursor.
Mus musculus (Mouse)
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Matches:
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SEQUENCE OF 1-31.
MEDLINE=78094475; PubMed=414225;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                precursors.";
                                                                                                                                                                                                                                MEDLINE=74170779; PubMed=4524622; Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.; Manhoo-acid sequence of the variable region of the heavy (alpha) chain of a mouse myoloma protein with anti-hapten activity."; Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
                                                                                                                                                                                                                                                                                                                                                                                         REVISION TO 53.

MEDLINE=77244979; PubMed=268248;
Hood L., Margolies M.N., Givol D., Zakut R.;
Unpublished results, cited by:
Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
-!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION MOPC 315.
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FRAMEWORK-4.
BY SIMILARITY.
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G -> H (IN REF. 2).
GY -> YG (IN REF. 4).
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                                                  SEQUENCE OF 1-21.
MEDLINE-79148758; PubMed=428562;
Schechter I., Wolf O., Zemell R., Burstein Y.;
"Structure and function of immunoglobulin genes and Fed. Proc. 38:1839-1845(1979).
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Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977)
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EMBL; X07880; CAA30727.1; -.
PIR; PL0102; AVMS35.
HSSP; P01825; 7F88.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00356; Ig_V.
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                                                                                                                GIGCAGCIACAGCAGTGGGGCGCAGGACTGITGAAGCCTICGGAGACCCTGTCCCTCACC 120
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                                                                                                                                      20 ValGinLeuGinGluSerGlyProGlyLeuValLysProSerGinSerLeuSerLeuThr
                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-8101213; PubMed-6774258;
Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
"Two types of somatic recombination are necessary for the generation of complete immunoglobulin heavy-chain genes.";
Nature 286:676-683 (1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                        AAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGA 348
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
         US-08-728-463B-205 (1-403) x HV60 MOUSE (1-116)
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PIR; A02094; GZMS14.
HSSP; POLBSE5; FTAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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Percent Similarity:
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P01819;
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STRAIN=BALB/CJ;
MEDIINE=8279149; PubMed=2499654;
A MEDIINE=8279149; PubMed=2499654;
I Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
I Levy N.S., malipiero U.V., Lebecque S.G., Gearhart P.J.;
The primary immune response.";
I Leprimary immune response.";
I SEXIV onset of 8007-2019(1989).
R NS EXP, PORSES; PRAB.
R InterPro; IPR003096; Ig_MGC.
R InterPro; IPR003096; Ig_V.
R Pfan; PF00047; ig; 1.
R Pfan; PF00047; ig; 1.
R SMART; SMO0406; IGV: 1.
R Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                     GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
15 heavy chain V region M315 precursor.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                 349 GTAATTAATTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEAVY CHAIN V REGION M315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13095 MW; 4562E03E53DC9E10 CRC64;
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75
15
25
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Conservative:
Mismatches:
Indels:
Gaps:
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FRAMEWORK-1
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI TaxID=10090;
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P18531;
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81 GlnLeuAsnSerValThrSerGluAspThrAlaThrTyrTyrCysThrSerLeu-----
                                                                                                                                                58 CAGGIGCAGCIACAGCAGIGGGGCGCAGGACIGITGAAGCCITCGGAGACCCIGICCCIC
                                                                                                                                                                                                                                                                                                                            CCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCCCTG
                                                                                                                                                                                                                                                                  178 CCAGGTAAGGGGCTGGAGTGGAATTGGGGAAATCATAGTGGAAGCACCAACTACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.; Elevy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.; Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response."; J. Exp. Med. 169:2007-2019(1989).
-!- MISCELLANBOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY. HSRP; PO1825; PRAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                358 TGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 ArgPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAla 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V REGION 1B43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW; 1CB547253681FF74 CRC64;
                  1113
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20
23
23
                                            Conservative:
Mismatches:
Indels:
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01-NOV-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
1G heavy chain V region 1B43 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ž
                Length:
Matches:
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                                                                                                                     US-08-728-463B-205 (1-403) x HV47_MOUSE (1-113)
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                                                                                           Gaps:
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MEDLINE=89279149; PubMed=2499654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL
                  .22e-26
                              354.00
78.26%
60.87%
47.64%
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116 AA;
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                                             Percent Similarity:
Best Local Similarity:
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   Alignment Scores:
Pred. No.:
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P18532;
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DISULFID
NON TER
SEQUENCE
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DB:
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No.:
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101 MetAenSerLeuGlnThrAspAspThrAlaArgTyrTyrCysAlaSerValSerIleTyr 120
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PIR, A02098, G2MS60.
HSSP, P01825; 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM0046; IGV; 1.
Immunoglobulin V region; Antiarsonate antibody.
NON TER 113 41; 12734 MW; 38DC0E0E3F5075B7 CRC64;
                                                                                                       TGCGCTGTCTATGGTGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCA
                                                                                                                                                                                                                      GGTAAGGGGCTGGAGTGGATTGGGGAAATCATAGTGGAAGCACCAACTACAACCCG
                                                                                                                                                                                                                                                                                                                         241 TCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCCCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                            TTC------GACCCCTGGGGCCAGGGAACCCTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
                                                                                                                                             GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Amino acid sequence of the heavy chain variable region from the A/J mouse anti-arsonate monoclonal antibody 36-60 bearing a minor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P01823.
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 JUR-1999 (Rel. 38, Last annotation update)
18 heavy chain V region 36-60.
Buka musculus (Mouse).
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
VCBI_TaxID=10090;
   38
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 AA
                                                        US-08-728-463B-205 (1-403) x HV43_MOUSE (1-144)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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STRAIN=A/J;
MEDLINE=84024551; PubMed=6414509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 22:4291-4296(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Juszczak E.C., Margolies M.N.;
51.39%
48.18%
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Best Local Similarity:
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                Query Match:
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136 GGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGTAAGGGGCTGGAG 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 SerGlyProGlyThrValLysProSerGluSerLeuArgLeuThrCysThrValSerGly 43
                                                                                                                                                                                                                                                                                              16 TICTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGCAGCTACAGCAG 75
                                                                                                                                                                                                                                                                                                                                  5 PhePheIlePheMetPhePheSerProSerCysIleLeuSerGlnThr---LeuGlnGlu 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 PheGluLeuSerSerTyrHisMetHisTrpileArgGlnProProGlyLysGlyLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 TGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 TrpileGlyValileAlaThrGlyGlySerThrAlaIleAlaAspSerLeuLyBABnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 GICACCATATCAGICGACACGICCAAGAACCAGITCTCCCTGAAGCTGAGCTCTGTGACC
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BEDDINE=89279149; PubMed=2499654;
Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early Onset of Somatic mutation in immunoglobulin VH genes during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                      IG HEAVY CHAIN V REGION XIG14
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BY SIMILARITY.
<1 18 135 IG HEAVY CHAIN V REGION XI
13 135
135 AA, 15080 MW; EBC467105C00732E CRC64;</pre>
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                                                                                                                                   Matches:
Conservative:
Mismatches:
Indels:
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01-NOV-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA
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J. Exp. Med. 169:2007-2019(1989).
PIR, JT0510, HVMS73.
HSSP; P01825; 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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                                                                                                                 2.73e-24
                                                                                                                                 336.00
65.91%
53.03%
45.22%
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                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                                                             Alignment Scores
Pred. No.:
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                                      NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                         61 GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
                                                                                                                                                                                                                                                                                                                                                    121 TGCGCTGTCTATGGTGGTCCTTC---AGTGGTTACTACTGGAGCTGGATCCGCCAGCCC 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88176921; PubMed-2451244;
Schwager J., Mikovyak C.A., Steiner L.A.;
"Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
from cDNA sequence: implications for evolution of immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGCTGAGCTCTGTGACCGCCGCGCACACGCCTGTGTATTACTGTGCGAGA 348
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71
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region XIG14 precursor (Fragment).
Xenopus laevis (African clawed frog).
                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 AA.
                                                                                                                                                    US-08-728-463B-205 (1-403) x HV61_MOUSE (1-116)
                                                                                                                 Gaps:
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InterPro, IPR003006, Ig_MHC.
InterPro, IPR01596, Ig_V.
Ffam, PF0047, ig_1 1.
SMART; SW00406; IGV, 1.
'Immunoglobulin V region; Signal.
NON_TER.
                5.82e-25
343.00
74.36%
60.68%
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PIR; B31933; B31933.
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                                                    Percent Similarity:
Best Local Similarity:
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Alignment Scores:
Pred. No.:
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                                                                                               Query Match
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Query Match: DB:

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81 LeuGlnMetSerLysValArgSerGluAspThrAlaLeuTyrTyrCysAlaArgLeuGly 100
                                                                                                                           58 CAGGIGCAGCIACAGCAGIGGGGCGCAGGACIGITGAAGCCTITCGGAGACCCTGTCCCTC 117
                                                                                                                                                                                                118 ACCTGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCC 177
                                                                                                                                                                                                                                                                                                                                                                                                         295 CTGAAGCTGAGCTCTGTGACCGCCGCGGACACGCCTGTGTATTACTGTGCGAGAGTA--- 351
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21 SerCysAlaAlaSerGlyPheAspPheSerArgTyrTrpMetSerTrpValArgGlnAla 40
                                                                                                                                                                                                                                                                                     235 AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCC 294
                                                                                                                                                                                                                                                                                                                                                                       61 ThrProSerLeuLysAspLysPhellelleSerArgAspAsnAlaLysAsnThrLeuTyr 80
                                                                                                                                               178 CCAGGTAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACC---AACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=64248078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
Tucker P.W.;
"Illegitimate recombination generates a class switch from C mu to C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 TyrTyrGlyTyrPheAspValTrpGlyAlaGlyThrThrValThrValSerSer 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352 ---ATTAATTGGTTCGACCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 402
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG HEAVY CHAIN V REGION TEPC 1017.
FRAMEWORK-1.
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FRAMEWORK-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        748157E4C6907B8E CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
PIR, A0203; HWNST7.
HSSP. PO1810; 2FBJ.
Interpro; IPR003006; Ig MHC.
     Conservative:
Mismatches:
Indels:
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                                                                                        US-08-728-463B-205 (1-403) x HV38_MOUSE (1-119)
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                                                          Gaps:
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SSP; P010810; 2Fbc.
InterPro; IPR003006; ...
InterPro; IPR003006; ...
InterPro; IPR003596; ig_v.
Pfam; PR0047; ig; 1.
SMART; SM00406; igv; 1.
SIGNAL 1 20
CHAIN 21 138 IG; ...
WAIN 21 49 FR
"WAIN 21 49 FR
"AIN 21 49 FR
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23-OCT-1986 (Rel. 02, Last seq
15-JUL-1999 (Rel. 38, Last ann
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   69.49%
55.08%
43.94%
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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P03980;
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Pred. No.:
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MEDLINE=79223895; PubMed=111245;

Rad D.N.; Rudikoff S., Krudzsch H., Potter M.;

Rad D.N.; Rudikoff S., Krudzsch H., Potter M.;

RT "Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and it spotential role in generating diversity in complementarity-determining regions.";

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THAT BINDS GALACTAN.

THAT BINDS GALACTAN.

PRESP, PO1810, 2FBJ.

InterPro; IPRO03006; Ig_WHC.

RISP PRO0407; ig; 1.

RINTERPRO, IPRO03596; Ig_V.

REAM; SMO0406; IGV: 1.

SWART; SMO0406; IGV: 1.
                                                                                                                                                                                                                                                                                                  GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
                                                                                                                                                                                                                                                                                                                                                                     121 TGCGCTGTCTATGGTGGGTCCTTCAGT-----GGTTACTACTGGAGCTGGATCCGCCAG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                            234
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                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                     20 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGlnSerIleAlaLeuThr 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 PheProGlyAsnLysLeuGluTrpileGlyTyrileTyrTyrSerAlaileThrSerTyr 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                        175 CCCCCAGGTAAGGGGCTGGAGTGGGGAAATCAATCATAGTGGAAGCACCAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGAAGCTGAGCTCTGTGACCGCCGCGGACACGCCTGTGTATTACTGTGCGAGA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                   13223 MW; 1595517827F976BE CRC64;
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                                                                                                         Conservative:
Mismatches:
Indels:
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                                                                      Length:
Matches:
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Matches:
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                                                                 2.16e-23
326.50
70.34%
57.63%
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326.50
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                  117 AA;
                                                                                                     Percent Similarity:
Best Local Similarity:
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HV38 MOUSE

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GCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCCCTGTTGTGGTGGGTCC 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 GGGGAAATCAAT---CATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGAGTC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 ACCATATCAGTCGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||:::::|||||||
88 ThrLeuThrValAspLysProSerSerThrAlaTyrMetGlnLeuSerSerLeuThrSer 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 GCGGACACGGCTGTGTATTACTGTGCGAGAGTA------ATTAATTGGTTCGAC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 AlaGluLeuValLysProGlyAlaSerValLysLeuSerCysLysAlaSerGlyTyrThr 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 GlyargileaspProAsnSerGlyGlyThrLysTyrAsnGluLysPheLysSerLysAla 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 CTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGGTGCAGCTACAGCAGTGGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region UPC10.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                    IG HEAVY CHAIN V REGION B1-8/186-2. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2. COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-83021113; PubMed-6181731; Auffray C., Sikorav J.L., Ollo R., Rougeon F.; "Correlation between D region structure and antigen-binding specificity: evidences from the comparison of closely related
                                                                                                                                                                                                                                                                 15419 MW; 1B57DD4FD0C9F465 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 TyrTrpGlyGlnGlyThrThrLeuThrValSerSer 139
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-UUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                             FRAMEWORK-3.
D SEGMENT.
JH2 SEGMENT.
BY SIMILARITY.
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                   Pfam, PF00047, ig, 1. --
SMART; SM00406, IGv, 1.
Immunoglobulin V region; Signal.
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67.42%
49.24%
43.41%
 InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                 139 AA;
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SEQUENCE FROM N.A.
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Best Local Similarity:
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                                                                                                                                                                                                          CAGIGGGGCGCAGGACTGITGAAGCCITCGGAGACCCTGTCCCTCACCTGCGCTGTCTAT 132
                                                                                                                                                                                                                                                                            GGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGTAAGGGGGCTG 192
                                                                                                                                                                                                                                                                                                                                                 GAGTGGATTGGGGAAATCAAT --- CATAGTGGAAGCACCAACTACAACCGTCCCTCAAG 249
                                                                                                                                                                                                                                                                                                                                                                                                                  AGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                      310 GTGACCGCCGCGCACACGGCTGTATTACTGTGCGAGA------GTAATTAATTGG 360
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                                                                                                                                                                                                                             5 TyrileileLeuPheLeuValAlaThrAlaThrAspValHisSerGlnValGlnLeuGln 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981)
-1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 402
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40
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                   Conservative:
Mismatches:
   Matches:
                                                                                                   US-08-728-463B-205 (1-403) x HV48_MOUSE (1-138)
                                                      Indels:
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HSSP; P01810; 2FBJ.
InterPib; IPR003006; Ig_MHC.
326.00
67.16%
49.25%
43.88%
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                Percent Similarity:
Best Local Similarity:
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                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swies Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs.sib.ch).
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immunoglobulin VH sequences.";
Ann. Immunol. (Paris) 132D:77-88(1981).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG GAMMA-2A MYELOMA
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-Dulayy chain V-II region SESS precursor.
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68 TrpLeuAlaArgIleAspTrpAspAspAspLysTyrTyrGlyThrSerLeuGluThrArg
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Takahashi N., Noma T., Honjo T.; "Rearranged immunoglobulin heavy chain variable region (VH) pseudogene that deletes the second complementarity-determining
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D SECHENT.
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                                                               Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984)
PIR; A02090; GRUCS.
HSSP; PO125; 7PBC;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR03596; Ig_V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 AACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACGACGTCCAAGAACCAG 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 GTAATTAATTGGTTCGACCCC----TGGGGCCAGGGAACCCTGGTCACCGTCTCTCA 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 MetAlaGlnValLysLeuGlnGlnSerGlyGlyGlyEeuValLysProGlyGlySerLeu 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lous musculus (Moduse).
Fukaryota, Metavoas, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
            MEDLINE=20183931; PubMed=10706631;
Shinohara N., Demura T., Fukuda H.;
Isolation of a vascular cell wall-specific monoclonal antibody
recognizing a cell polarity by using a phage display subtraction
method.";
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                 E0F96B8A17004317 CRC64;
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Last sequence update)
Last annotation update)
2a (Fragment).
                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000)
EMBL; AB036341; BAA88633.1; -.
HSSP; PO1607; HREI.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
Ffam; PP00047; ig; 2.
SMART; SMO064; IGv; 2.
SEQUENCE 298 AA; 31867 MW; E0P96BBA17004317 (
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Matches:
Conservative:
Mismatches:
Indels:
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STRAIN=BALB/C; TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                           1.87e-26
343.00
65.71%
52.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21, Anti-MOG Z12 variable gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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DB:
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61 GIGCAGCTACAGCAGTGGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                                                                                                                                                                                                        NON TER 168 168
SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;
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68
21
45
45
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Matches:
Conservative:
Mismatches:
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PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
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Sembi P.;
"Targeting T cells to the CNS.";
"Targeting T cells to the EMBL/Ge.
EMBL; AA416332; CAC94867.1;
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.MHC.
InterPro; IPR001230; Prenyl_site.
Pfam; PP00047; Ig.
SWART; SM00409; IG; I.
SWART; SM00409; IG; I.
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336.00
64.49%
49.28%
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Job time: 38.7747 secs
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Best Local Similarity:
Query Match:
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GIGCAGCTACAGCAGTGGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CN 8 scFv.
CN 8.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 11.
CNEL TaxID=10090;
        Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC018115; AAH18315.1; -
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003506; Ig_N.
InterPro; IPR00407; Ig_S.
InterPro; IPR00409; Ig_S.
SWART; SW00409; IG, 2.
SWART; SW00409; IG, 2.
SWART; SW00409; IG, 1.
FROSITE; PS00290; IG MHC; UNKNOWN_3.
Hypothetical protein.
SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
                                                                                                   EMBL/GenBank/DDBJ databases
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71
21
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Matches:
Conservative:
Mismatches:
Indels:
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67.15%
51.82%
47.58%
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                                                  SEQUENCE FROM N.A.
TISSUE=SALIVARY GLAND;
                                                                                 Strausberg R.;
Submitted (DEC-2001)
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Best Local Similarity:
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SEQUENCE FROM N.A.
                   NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||| ||| ||| ::: |||| ||| CVSThrValSerGlyPheAlaLeuThrSerTyrAlaIleSerTrpValArgGlnProPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 67.9 kDa protein.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GluGlyAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 137
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                                                                                                                                                                                                                                                              Streamberg R.;
Streamberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; PC011181; AAH11181.1;
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC7F3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               482
75
18
41
3
                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (protein for MGC:18822).
                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                 482 AA
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355.50
67.88%
54.74%
47.85%
                                                              PRELIMINARY;
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SerSer 122
                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                              Q91X92;
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DB:
                                                            Q91X92
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AGA-----GTAATTAATTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTC 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||||||||||::: ||| ||| ||| ThrCysAlallaAlaTrpAsnTrpIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCTGCGCTGTCTATGGTGGGTCCTTCAGT-----GGTTACTGGAGCTGGATCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 ACCAACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAAC
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                                                                                                                                                                                                                                                       X MEDLINE-98277139; PubMed=9614934;
X MEDLINE-98277139; PubMed=9614934;
A Volug D.C.;
T "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
R EMBL, APO35039, AAD56275.1; -..
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003006; Ig_WHC.
R SWART; SM00406; Ig_V.
R SWART; SM00406; Ig_V.
T NON_TER 12 122
C SEQUENCE 122 AA, 13719 MW; 56CB0612586A6529 CRC64;
                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                         355 AATTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
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75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.26e-28
363.50
73.77%
61.48%
                                                                                                     PRELIMINARY;
                                                                                                                                                                                           Homo sapiens (Human)
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Best Local Similarity:
                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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            CTGAAGCTGAGCTCTGTGACCGCGGGCACACGCTGTGTATTACTGTGCGAGA----- 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCGCTGTCTATGGTGGTCCTTC---AGTGGTTACTACTGGAGCTGGATCCGCCAGCCC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGGTAAGGGCCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTACAAC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCCCTG 297
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| CysSerValThrGlyTyrSer1leThrSerGlyTyrTyrTrpAsnTrp1leArgGlnPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                            ---GIAATTAATTGGTTCGACCCCTGGGCCAGGGAACCCTGGTCACCGTCTCC
                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002091; AAH02091.1; -.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
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88
16
29
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Matches:
Conservative:
Mismatches:
Indels:
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INCEPPO; IPR003599; IG.
INCEPPO; IPR003500; IG_11ke.
INCEPPO; IPR003500; IG_11ke.
INCEPPO; IPR003506; IG_MHC.
INCEPPO; IPR003596; IG_W.
Fam, PF00047; IG; 3.
SWART; SW00409; IG; 3.
SWART; SW00406; IGV; 1.
SWART; SW00410; IG 1ke; 1.
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430.50
76.47$
64.71$
57.94$
                                                                                                                                         PRELIMINARY;
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SEQUENCE FROM N.A.
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DB:
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ACCTGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCC 177
                                                                               CCAGGTAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTACAAC 237
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|ThrCygThrValSerGlyGlySerIleCysSerTyrTyrTrpSerTrpIleArgGlnPro 40
                                                                                              61 GTGCAGCTACAGCAGTGGGGGGGCGCAGGACTGTTGAAGCCTTTCGGAGACCCTGTCCCTCACC 120
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      CCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACGTCCAAGAACCAGTTCTCCCTG
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|TrpGlyProTyrTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                Strauberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025985; AAH125985.1; -.
Hypothetical protein:
SEQUENCE 473 AA; 51986 MW; E29920B03BA369F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
11-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypotherical 52.0 kbs protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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490.50
78.99%
70.29%
66.02%
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TISSUE=KIDNEY;
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Best Local Similarity:
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                                       118
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                                                                                                                                                                           TGCGCTGTCTATGGTGGTCCTTC----AGTGGTTACTACTGGAGCTGGATCCGCCAG 174
                                                                                                                                                                  294
                                                                                                                                                                                                                   ------GTAATTAGTTCGACCCCTGGGGCCAGGGAACCCCTGGTCACC 393
                                                                                                                                                                                                                                                              121 TyrSerArgSerGlyArgThrGlyAlalleAbpTyrTrpGlyGlnGlyThrLeuValThr 140
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41 CysThrValSerGlyGlySerIleSerSerSerSerTyrTyrTyrGlyTrpIleArgGln
                                                                                                                   AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCC
                                 GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC
                                                                                                                                                                                                        CTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTTATTACTGTGCGAGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Myosin-reactive autoantibodies in rheumatic carditis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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85.71%
79.83%
66.08%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Best Local Similarity:
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Young D.C.
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                                  61
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Q9UL73;
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NON TER
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CAGGTGCAGCTACAGCAGTGGGGGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTC 117

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61 GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MetGlyAlaPheAspPheTrpGlyHisGlyThrMetValThrValSerSer 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC016369; AAH16369.1; -. InterPro; IPR003006; Ig_MHC.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 53.4 kba protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                 Conservative:
Mismatches:
Indels:
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                                                                                                                                       Gaps:
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                                                                                                                                                                              US-08-728-463B-205 (1-403) x 095973 (1-150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prem. Prond. 19, 4. Prem. Prond. 19, 4. PROSITE, PS00290; IG MHC, UNKNOWN_1. Hypothetical protein. SEOUENCE 496 AA; 53391 MW, D3469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.95e-45
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78.328
74.138
70.598
                                              553.50
86.86%
78.83%
74.50%
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Best Local Similarity:
                                                                   Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
      Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluLeuProThrValGlyLeuPheTyrTrpGlyGlnGlyThrLeuValThrValSerSer 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                 21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 CysThrValSerGlyGlySerIleSerSerTyrTyrTrpSerTrpIleArgGlnProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTACAACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

A Sub C.-H., Song C.-H., Lee C.-H., Lee S.-K.;

Sub C.-H., Song C.-H., Lee C.-H., Lee S.-K.;

I "Clonal proliferation of IgM secreting B cell in the synovium of Behcet's patient with arthritis.";

L Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

R EMBL; APT03795; AAC79084.1;

R PRSP; PO1925; 7FAB.

R InterPro; IPR003006; Ig MHC.

R InterPro; IPR003596; Ig_V.

R Pfam; PF00047; ig; 1.

R SMRRT; SM00406; IGV; 1.

R SIGNAL

I SIGNAL
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VH4 HEAVY CHAIN VARIABLE REGION.
PROSITE; PS00290; IG MHC; UNKNOWN_3.
Immunoglobulin domain.
SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW; 85664E04938AA7C9 CRC64;
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1115
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
VH4 heavy chain variable region precursor (Fragment)
                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                       US-08-728-463B-205 (1-403) x Q96EY0 (1-613)
                                                                                                        6.12e-50
573.50
84.29%
82.14%
77.19%
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Best Local Similarity:
                                                                                          Alignment Scores:
Pred. No.:
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NON TER
SEQUENCE
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ol-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRA-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (protein for MGC:20337).
Unknown (protein for MGC:20337).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AAH11857.1; -.
InterPro; IPR003598; Ig_c2.
InterPro; IRR003006; Ig_MHC.
Pfam; PF00047; ig; 5.
SMART; SM00408; IGc2; 2.
                            597
124
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10
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                      4.84e-57
643.00
86.11%
86.11%
86.54%
         InterPro; IPR003596; Ig_v.
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141 ThrValSerSer 144
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Best Local Similarity:
Query Match:
DB:
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TISSUE=B-CELL;
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096EY0
1D 096E
AC 096E
AC 096E
DT 01-D)
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Q9BQBB;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Unknown (protein for MGC:1905) (protein for MGC:1228).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE=MUSCLE;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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  96DBD4C7C696E0A6 CRC64;
                                                                          618
125
0
9
10
                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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618 AA; 67758 MW;
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SEQUENCE FROM N.A.
TISSUE-LYMPH;
Straubberg R.;
Submitted (JAN-2001) to the EWEMBL; BC006180; AAH06180.1;
HSEP; P01825; 7FAB.
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InterPro; IPR003597; Ig. cl.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
                                                                   1.19e-57
649.00
86.81%
86.81%
87.35%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 ACCGTCTCCTCA 402
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141 ThrValSerSer 144
                                                                                      Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                             Alignment Scores:
SEQUENCE
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                                                                     Pred. No.:
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240

80

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40

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300

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61 GTGCAGCTACAGCAGTGGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCCCCTGAAG 300
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017356; AHH17356.1; -.
InterPro; IPR003598; Ig c2.
InterPro; IPR003506; Ig_MHC.
Pfam; PR0047; Ig; 5.
SMART; SM00408; IGc2; 1.
PROSITE; PS00290; IG MHC; UNKNOWN 3..
Hypothetical protein; Immunoglobulin domain.
SMART; SM00407; IGC1; 4.

SMART; SM00406; IGV; 1.

SMART; SM00410; IG like; 1.

PROSITE; PS00290; IG MHC; UNKNOWN_3.

PROSITE; PS01290; IG MHC; UNKNOWN_3.

SEQUENCE 597 AA; 65274 MW; 2DAFABFB7E055851 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 67.8 kDa protein.
                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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TISSUE=LYMPH;
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Pred. No.:
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 65.3 kDa protein.
Hypothetical 65.3 kDa protein.
Hypothetical 65.3 kDa protein.
Hypothetical 65.3 kDa protein.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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P SEQUENCE FROM N.A.

A Strausberg R.;
Strau
   SMART; SMO0406; IGV; 1.
PROSITE; PS00239; IG MHC; UNKNOWN_3.
Hypothetical protein.
SEQUENCE 588 AA; 64438 MW; FCGODBAD82B39FD7 CRC64;
                                                                                                                                                                                                      588
125
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
Query Match:
DB:
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Q8wukl homo sapien
Q924p8 mus musculu
Q921k1 mus musculu
Q92c77 homo sapien
Q95pg4 mus musculu
Q95cb9 homo sapien
Q94q1 mus musculu
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Q8vcx7 mus m
Q9qyf0 mus m
Q8vdc9 mus m
Q9d814 mus m
Q9wukl homo s
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Q924r6 mus m
Q924r0 mus m
Q9u194 homo s
Q9u190 homo s
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Q9ul75 homo
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019235, AAH19235.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.cl.
InterPro; IPR003596; Ig.Mrc.
InterPro; IPR003596; Ig.W.
Pfam; PF00047; Ig; 5.
SMART; SM00409; IG; 2.
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Last annotation update)
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         Q96AA6
Q96BB
Q96EY0
Q96EY0
Q96EXB
Q9UL/3
Q8UCG3
Q9UL/5
Q9UL/5
Q9UXQQQQYF0
Q9UCXY
Q9UCXY
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Q9UCXY
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Q924 P8
Q921K1
Q91777
Q96K68
Q99NG4
Q924R3
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Q924Q8
Q924Q0
Q924Q7
Q924R8
Q924R7
Q91VA2
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Q8W224
Q924P9
Q924R9
Q924R2
Q924R6
Q924R6
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01-MAR-2002 (TrEMBLrel. 20, La
01-JUN-2002 (TrEMBLrel. 21, La
Hypothetical 64.4 kDa protein
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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Q8WUX4
3, 2003, 08:56:26 ; Search time 35.7747 Seconds (without alignments) 4642.224 Million cell updates/sec
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                                                                                     US-08-728-463B-205
743
1 ATGAAACACCTGTGGTTCTT......CCTGGTCACCGTCTCCTCAG 403
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   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                    - protein search, using frame_plus_n2p model
                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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Sequence 17, Apply Sequence 17, Apply Sequence 934, Apply Sequence 954, Apply Sequence 1316, Apply Sequence 1622, Apply Sequence 1626, Apply Sequence 1626, Apply Sequence 5, Apply Sequence 5, Apply Sequence 1578, Apply Sequence 1559, Apply 
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Sequence 1339, App
Sequence 1360, App
Sequence 990, App
Sequence 50, Appl
Sequence 1619, App
Sequence 841, App
Sequence 1619, App
  Sequence 145, App
Sequence 162, Ap
Sequence 1313, Ap
Sequence 1659, Ap
Sequence 1413, Ap
Sequence 17, Appl
Sequence 12, Appl
Sequence 4, Appli
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Sequence 1651, Ap
Sequence 44, Appl
Sequence 1994, Ap
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Sequence 971, App
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JULIE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF5.3

CURRENT APPLICANTON NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2000-10-17

PRIOR PILING DATE: 2001-03-16

PRIOR PILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE PATENTIN VET: 2.0
0 US-09-800-729-145
US-09-880-748-1642
US-09-880-748-1633
US-09-880-748-1633
US-09-880-748-1413
US-10-211-357-18
US-10-211-357-10
US-10-211-357-12
US-10-211-357-12
US-09-86-4298-4
US-09-86-4298-4
US-09-86-761-44315
US-09-86-761-44315
US-09-880-748-1326
US-09-880-748-1326
US-09-880-748-1316
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US-09-880-748-1316
US-09-880-748-1318
US-09-880-748-1319
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US-09-925-299-971
US-09-925-299-971
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US-09-980-748-1330
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US-09-880-748-1651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1321, Application US/09880748; Publication No. US20030059937A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
US-09-880-748-1321
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LENGTH: 249
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                                                                                 Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/Cogn1/US08728463/runat_03062003_085618_16959/app_query.fasta_1.3690
-Q=/Cogn2_1/USPTO_epool/US08728463/runat_03062003_085618_16959/app_query.fasta_1.3690
-DB=Published Applications AA -QFWT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNIT$=bits -START=1 -END=-1 -MATRIX=blosum62
-TRAMS=human40.cdi -LIST=45 -DOCALIGN=200 -THR MAXE=10
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US08728463_@CGN 1 1 51 @runat_03062003_085618_16959
-NCPUe= CICPD=3 -NO MMAP -LARGRQUERY* NEG $GORES=0 - WAIT -DSPBLOCK=100
-LONGLOG -DBY $IMBCUT=120 - WARN TIMBCUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 - YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 957, App
Sequence 12, Appl
Sequence 12, Appl
                                                                                                                                                                             3, 2003, 09:04:15 ; Search time 17.1229 Seconds (without alignments) 4764.744 Million cell updates/sec
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                                                                                                                                                                                                                                                                                  US-08-728-463B-205
743
1 ATGAAACACCTGTGGTTCTT......CCTGGTCACCGTCTCCTCAG 403
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/ cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

/ cgn2_6/ptodata/1/pubpaa/NEV6_NEW_PUB.pep:*

/ cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

/ cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

/ cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

/ cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

/ cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

/ cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                     - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-880-748-1321
US-09-880-748-957
US-10-124-905-12
US-09-948-429B-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383519 segs, 101223694 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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74.2
74.2
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Database

Score

Result No.

588.5 555.5 551 551

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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                            178 CCAGGTAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTACAAC 237
                                                                                                                                                                                                                                                                                                                                                          81 LysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgValGlyLeu 100
                                                                                                                                        118 ACCTGCGCTGTCTATGGTGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                         ------GACCCTGGGGCCAGGGACC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 ThrCysAlaValTyrGlyGlySerPheSerAsnTyrTrpSerTrpIleArgGlnPro
                                                                                                                                                                                                                                 CCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCCCTG
                          US-08-728-463B-205 (1-403) x US-09-880-748-957 (1-249)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-70W-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    358 TGGTTC------
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// Patent No. US20020166136A1
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC OPERATING SYSTEM:
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J APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PES23

CURRENT APPLICATION WUMBER: US/09/880,748

CURRENT FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR PELICATION NUMBER: 60/277,379
PRIOR PELICATION NUMBER: 60/277,379
PRIOR PELICATION NUMBER: 60/277,379
PRIOR PELING DATE: 2010-03-21
PRIOR PELING DATE: 2010-03-21
PRIOR PELING DATE: 2010-05-25
NUMBER OF SEC ID NOS: 22:0
SOFTWARE: PATENTIN VOR: 22:0
SOFTWARE: PATENTIN VOR: 22:0
LENGTH: 249
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                                                         Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
                       Length:
Matches:
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Publication No. US20030059937A1
GENERAL INFORMATION:
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                                                       89.68%
88.89%
79.21%
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88.10%
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74.76%
                                                  Percent Similarity:
Best Local Similarity:
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Query Match:
DB:
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US-09-880-748-957
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Alignment Scores:
Pred. No.:
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61 GTGCAGCTACAGCAGTGGGGCGCAGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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Mismatches:
Indels:
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TITLE OF INVENTION: 32 Human secreted proteins
FILE REPERBNCE: PZ044Pl
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                 FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-5021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 145, Application US/09800729
Patent No. US20020068319A1
GENERAL INFORMATION:
              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 CTGGTCACCGTCTCCTCA 402
                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                          4.23e-43
551.00
81.51%
76.03%
74.16%
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                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                    linear
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Best Local Similarity:
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Patent No. US20020177689A1

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS ITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREEL: 699 Prince Street

CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGAAGCTGAGCTCTGTGACCGCCGCGCACACGCCTGTGTATTACTGTGCGAGA----- 348
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                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:
                                                                                                                       Matches:
Conservative:
Mismatches:
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551.00
81.51%
76.03%
                               MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
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TYPE:
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                                                                                                        Pred. No.:
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234

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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN VEY. 2.0
SEQ ID NO 1642
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SEQ ID NO 1333
LENGTH: 253
                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1642
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ORGANISM: Homo sapiens
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Best Local Similarity:
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
FRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
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Matches:
Conservative:
Mismatches:
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        PCT/US00/26013
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Publication No. US20030059937A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: PCT/US
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 145
LENGTH: 487
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548.50
80.95%
74.83%
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Best Local Similarity:
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                                                                                                                                        TYPE: PRT
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FILE REPRENCE: FF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT APPLICATION NUMBER: US/09/880,748
FRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-66-15
PRIOR PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-06-25
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    255
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                        Matches:
Conservative:
Mismatches:
Indels:
       Length:
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Publication No. US20030059937A1
GENERAL INFORMATION:
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                                                                                                                                                       Sequence 1413, Application US/0980748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; TIME REPERENCE: PPS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
; PRIOR PILING DATE: 2000-10-17
; PRIOR PILING DATE: 2000-10-17
; PRIOR PILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-16
; PRIOR PILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PATENTIN Ver. 2.0
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Conservative:
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US-09-880-748-1413
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Best Local Similarity:
Query Match:
DB:
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Mismatches:
Indels:
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Matches:
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ORGANISM: Homo sapiens
US-09-880-748-1659
                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-880-748-1333
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Pred. No.:
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121 TOCGCTOTCTATGGTGGGTCCTTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCC 177
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Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCC
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Mismatches:
Indels:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <a href="https://documer.com/chas-ariginal-application">CLASSIFICATION: <a href="https://documer.com/chas-ariginal-applic
                                             Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, STREET: 699 Prince Street
CITY: Alexandria
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity:
Alignment Scores:
Pred. No.:
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Reff, Mitchell B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
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107
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Matches:
Conservative:
Mismatches:
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               012712-165
                                                                                                                                                                                                                                                          Indels:
                                                                                                      TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECK
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER REABALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
REGISTRATION NUMBER: 35,030
REPERBUCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAK: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/10211357
Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
                                                                                            LENGTH: 467 amino acids
                                                                                                                                                                                                     1.61e-41
534.00
82.86%
76.43%
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Best Local Similarity:
Query Match:
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US-10-211-357-12
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Patent No. US20020166136A1
GENERAL INPORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr
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Version
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                             FILING DATE: 05-Aug-2002
CLASSIFICATION: «UDKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-7ul-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 467 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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534.00
82.86%
76.43%
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Best Local Similarity:
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US-10-124-905-4
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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                               121 ArgProAspCysThrThrIleCysTyrGlyGlyTrpValAspValTrpGlyProGlyAsp 140
                  ---GTAATTAATTGGTTCGACCCCTGGGGCCAGGGAACC 384
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107
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12
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION NUMBER: 05/09/940,429B
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE: 07-0W-1995
FILING DATE: 07-0W-1995
ATTOCNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,031
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape:
                                                                                                                                                                                       Sequence 4, Application US/09948429B; Patent No. US20020177689A1; GENERAL INFORMATION:
                                                                                                       385 CTGGTCACCGTCTCCTCA
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534.00
78.08%
73.29%
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                                                                                                                                                                        US-09-948-429B-4
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DB:
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       PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF IMMUNOSUPPRESANTS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 CCAGGTAAGGGGCTGGAGTGGATTGGGGAAATCAATCATGGA---AGCACCAACTAC 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ProGlyArgGlyLeuGluTrplleGlyHisileTyrGlyAsnGlyAsnThrAsnTyr 80
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107
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12
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              012712-131
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Teskin, Robin L. REGISTARION NUMBER: 35,030 REFERENCE/DOCKET NUMBER: 012 TELECOMMUNICATION INFORMATION:
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534.00
78.08%
73.29%
71.87%
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 LeuSerLeuThrCysAlaValTyrGlyGlySerPheSerGlyTyrTyrTrpSerTrpIle 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 CIGICCCTCACCTGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                       2.00e-57
                                                                                                                                                                                                                                                                                     OTHER INFORMATION: MAP TO AB019439.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.57
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.55
OTHER INFORMATION: EST HUMAN HIT: BE672445.1, EVALUE 2.00.
US-09-864-761-44310N: SWIËSPROT HIT: P06331, EVALUE 1.00e-53
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                    PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Job time : 20.1229 secs
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530.00
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Best Local Similarity: %100.00%
Query Match: 71.33%
DB:
                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                     SEQ ID NO 44315
LENGTH: 117
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
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Sequence 634

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TGCGCTGTCTATGGTGGTCCTTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCC 177
                                                                                                                                CCAGGTAAGGGGCTGGAGTGGATTGGGGAAATCATAGTGGA---AGCACCAACTAC 234
                                                                                                                                                                                                                                                                                                                                                                                                 CTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGA---- 348
                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ArgProAspCysThrThr1leCysTyrGlyGlyTrpValAspValTrpGlyProGlyAsp 140
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                                      PRIOR PELICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-08-05
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PELING DATE: 2001-01-30
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PEDLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
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Best Local Similarity:
Query Match:
DB:
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; Patent No. 6312690
; TAPLICANT: EBELMAN, LENA
; APPLICANT: EACOREM, MICHEL
; APPLICANT: CHABEHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; TITLE OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
FILING TAXES OF 
INFORMATION FOR SEQ ID NO: 118:
                                                                                                                                                                                                                                                            4.01e-60
622.00
100.00%
100.00%
83.71%
                         SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-118
                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
D8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 PheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTrpIle 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 GCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTATGGTGGGTCC
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GENERAL INCOMMATION:
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: A-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 TGGTTCGACCCCTGGGGCCAGGAACCCTGGTCACCGTCTCCTCA 402
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Matches:
Conservative:
Mismatches:
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                                                                                      660-118-0 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application US/09049672A; Patent No. 6135941
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: 0BLON, NORMAN 24, 618
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-1
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-413-220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
                                                                                                                                                                                                                                                                                                                                         1.27e-56
592.00
86.67%
84.44%
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Sequence 4, Appli
Sequence 6, Appli
Sequence 108, Appl
Sequence 108, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 123, Appli
                                                                                                                                                                                                                                                                                                                                     114, App

53, Appl

53, Appl

73, Appl

16, Appl

11, Ap
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APPLICANT: Matguda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 79,
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Sequence 3
Sequence 6
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                                 STATE: MOSTON
STATE: MOSTON
STATE: MOSTON
ZIP: 02110-2804
COUNTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASELEG for Windows95
FILING DATE: 27-MAR.1993
ATTORNEY/AGENT INFORMATION:
NAME: FREEMENT INFORMATION:
NAME: FREEMENT INFORMATION:
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-8906
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225 Franklin Street
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CITY: Boston
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TELEX: 20
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      Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/Capl 1/USG9728FO spool/USG9728463/runat 03062003 085615 16867/app_query.fasta_1.3690
-DB=Issued_Patente_AA -OFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pto -NORM=ext -HARPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=LOCAL -OUTFWT=pto -NORM=ext -HARPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=USG9728463 @CGN 1 1.97 @runat 03062003 085615 18667 -NCPU=6 -ICPU=3
-NO MWAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGICG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 140, Appl
Sequence 142, Appl
Sequence 92, Anni
                                                                                                                                                                                                      3, 2003, 09:02:35 ; Search time 9.17299 Seconds (without alignments) 2585.294 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGAAACACCTGTGGTTCTT......CCTGGTCACCGTCTCCTCAG 403
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             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/pCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pCTUS_COMB.pep:*
                                                                                                                                         protein search, using frame_plus_n2p model
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US-08-793-450-8
US-08-793-450-4
US-08-793-450-4
US-08-480-774A-2
US-08-487-550-12
US-08-545-809A-142
US-08-545-809A-142
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US-08-523-894-10
US-08-523-894-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                        US-08-728-463B-205
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Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                            June
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7.77.9
7.74.0
7.25.0
7.17.9
7.1.9
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Perfect score:
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                                                                                                                                                                                                         Run on:
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No.
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58 CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTC 117
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                                                                                 GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITE, CHRISTEL
APPLICANT: MACACOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                   ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
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109
109
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 03-SEP-1994
ATTORNEY/AGBNT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Mismatches:
Indels:
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Matches:
    RESULT 4
US-08-793-450-4
Sequence 4, Application US/08793450
Patent No. 6312690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.68e-55
578.00
90.24%
88.62%
77.79%
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCC 294
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118
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Matches:
Conservative:
Mismatches:
Indels:
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                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION 15.36
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY, AGENT INPORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650-855-0555
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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578.50
86.01%
82.52%
77.86%
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LENGTH: 473 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity:
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US-09-049-672A-4
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ADDRESSE: BURNS, DOADE, SECRET STATES OF THEREOF AS STREET: 699 Prince Street ADDRESSED FORMS THEREOF AS STREET: 699 Prince Street ADDRESSED FORMS THEREOF AS TITLE OF INVENTION: TO HUMAN BY.1 AND/OR BT.2 PRIMATIZED FORMS THEREOF AS TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS"

CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Abanadria
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                                                                                                                                                                                                                                            TGCGCTGTCTATGGTGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCA 180
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                                                                                                                                                                                                                                                                     41 CysThrValSerGlyGlySerIleSerSerHisTyrTrpSerTrp1leArgGlnSerPro 60
                                                                                                                                                                                                                                                                                                                                            61 GlyLysGlyLeuGlnTrpIleGlyTyrIleTyrTyrSerGlySerThrAsnTyrSerPro 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AlaValPheTyrGlyAspTyrArgLeuAspProTrpGlyGlnGlyThrLeuValThrVal 140
                                                                                     1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
                                                                                                              181 GGTAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTACAACCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
                                          US-08-728-463B-205 (1-403) x US-08-480-774A-2 (1-142)
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.......: US/08/487,550
07-JUN-1995
1N: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 TCCTCA 402
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141 SerSer 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-487-550-12
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APPLICANT: SOBROSKI, Joseph G.
APPLICANT: HASELTINE, William A.
APPLICANT: POSNER, Marshall R.
TITLE OF INVENTION: REACTIVE NEUTRALIZING HUMAN
TITLE OF INVENTION: ANTI-GP 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME
TITLE OF INVENTION: AND USE THEREOF
                                                                                                                                            393
                                                                                                                                                             101 TyrLysTrpLysTyrHisGlyAspTrpPheAspProTrpGlyGlnGlyThrThrValThr 120
61 ProSerLeuLysSerArgValThrileSerValAspThrSerLysAsnGlnPheSerLeu 80
                                                                                 355 ------AATTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
130 Water Street
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Matches:
Conservative:
Mismatches:
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OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
OSCHWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,774A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/400,674
FILING DATE: 08-MAR-1995
APPLICATION NUMBER: 07/804,652
FILING DATE: 10-DEC-1991
ATTONEY/ABENT INFORMATION:
NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08480774A
Patent No. 5852186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.48e-54
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85.92%
77.46%
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LENGTH: 142 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-523-6440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein FRAGMENT TYPE: internal
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ADDRESSEE: DIKE, BRC
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                          394 GICTCCICA 402
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Best Local Similarity:
Query Match:
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US-08-480-774A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGGTAAGGGGCTGGAGTGGGGAAATC---AATCATAGTGGAAGCACCAACTAC 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GTAATT-----AATTGGTTCGACCCCTGGGGCCAGGGAACC 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCES: 145
CORRESPONDENCE ADDRESS:
                                                                                                 476
1111 8
8 15
12
                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                            US-08-728-463B-205 (1-403) x US-08-487-550-12 (1-476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDESCREE: 225 Franklin Street
CITY: Boston
STREET: 225 Franklin Street
CITY: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows95
SOFTWARE: YOUNDER: US/08/545,809A
FILING DATE: 27-MAR.1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-545-809A-140
; Sequence 140, Application US/08545809A
; Patent No. 6096878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 CTGGTCACCGTCTCTCA 402
                                                                                               3.91e-52
551.00
81.51%
76.03%
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                Alignment Scores:
Pred. No.:
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DB:
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121 TGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCA 180
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APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 CTGAGCTCTGTGACCGCCGCGGACACGCCTGTGTATTACTGTGCGAGA 348
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Conservative:
Mismatches:
Indels:
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                                                                      29,066
ER: 06501/004001
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PCT/JP93/00603
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                                                                                                                           TELERAX: 617-5-
TELEX: 200154-7-
TELEX: 200154-7-
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
"VPE: amino acids
                                                     NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 0650
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-8906
               FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
                                                                                                                                                                                                                                                                                                                                                            3.05e-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: Window
                                                                                                                                                                                                                                                                                                                                                                            550.00
93.10%
90.52%
74.02%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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STREET: 22.
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US-08-545-809A-142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 95. Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Honjo, Tasuku
APPLICANT: MATEUGA, Fuminiko
TITLE OF INVENTION: HUMAN iMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCE ADDERSS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGG
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Conservative:
Mismatches:
FastSEQ for Windows Version 2.0
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       CURRENT AREL: FASESE (100 WINDOWS VEFSION CURRENT AREL: FASESE (100 WARS)

APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTONNEY AGENT INPORMATION: NAWE: Freeman, John W. REGISTRATION NUMBER: 29,066
REFERENCE DOCKET NUMBER: 06501/004001
TELEPHONE: 617-542-6070
TELEPHONE: 617-542-8906
TELEPAX: 200154
INFORMATION FOR SEQ ID NO: 142: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         LENGTH: 118 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                            539.00
91.53%
88.98%
72.54%
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                         TYPE: ami
TOPOLOGY:
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STATE: MA
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61 GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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APPLICANT: Hanna, Nabil
APPLICANT: Reff, Mitchell B.

APPLICANT: Reff, Mitchell B.

APPLICANT: Reff, Mitchell B.

TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human TITLE OF INVENTION: Therapy

NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 CTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGA 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/55,809A
FILING DATE: 27-MAR-1996
PILING APPLICATION DATA:
APPLICATION NUMBER: DCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
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Patent No. 6136310
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538.00
91.38%
88.79%
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity:
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DB:
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ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                          35,030
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                             COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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82.86%
76.43%
71.87%
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                                                                                                                                                Alexandria
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467
107
9
                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE: 06-SEP-1995
CLASSIFICATION: 424
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Mismatches:
Indels:
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                   BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
                                                                                                                                                                                                                                  ATTORNEY/ACENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFESTRENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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US-08-523-84-10
; Sequence 10, Application US/08523894
; Patent No. 6136310
                                                                                                                                                                                                                                                                                                                  TELEFAX: 703-836-202.
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 467 amino acids
TYPE: amino acid
                                                               SIGNAL:
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
TYPE: Floppy disk
                            : 699 Prince Street
Alexandria
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82.86%
76.43%
71.87%
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CORRESPONDENCE ADDRESS:
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Best Local Similarity:
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Pred. No.:
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APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467
107
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18
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                                                                                                                                                                                                                                                                                                                                                            COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
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Matches:
Conservative:
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESANTS"
                                                                                       101 LeulysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaSerAsn11e 120
                                                                                                                                                        121 LeubysTyrLeuHisTrpLeuLeuTyrTrpGlyGlnGlyValLeuValThrValSerSer 140
          81 AsnProSerLeuAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100
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                                                                                                                                 346 --- AGAGTAATTAATTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
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Matches:
Conservative:
Mismatches:
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699 Prince Street
                                                CTGAAGCTGAGCTCTGTGACCGCCGCGGACACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-UIN-1995
                                                                                                                                                                                                                                                    Sequence 4, Application US/08487550
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,0
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78.08%
73.29%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 699 Princ
CITY: Alexandria
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                                                                                                                                                                                                                                                                       Patent No. 6113898
GENERAL INFORMATION:
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DB:
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121 LeulysTyrLeuHisTrpLeuLeuTyrTrpGlyGlnGlyValLeuValThrValSerSer 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
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                                                                                                                                                               APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: APENICATION DATA:

APPLICATION NUMBER: US/08/523,894

FILING DATE:

APPLICATION AND ATA:

APPLICATION NUMBER: US/08/523,894
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Indels:
                                                                                                                                                                                                                                                                                                      ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                   Sequence 12, Application US/08523894
Patent No. 6136310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 467 amino acids TYPE: amino acid
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82.86%
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                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
ADDRESSEE: BURNS, DO
                                                                                                                                         GENERAL INFORMATION:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 0. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                US-08-523-894-12
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                                                                                                                                                                                                                                                                                                                                                                      STATE: V. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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: 134 amino acids
amino acid
3Y: linear
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84.21%
74.44%
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                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ర
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                                                                                                                                    US-08-259-372A-6
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US-08-468-671-6
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                                                                                                                                                                                                          ----GTAATTAATTGGTTCGACCCCTGGGGCCAGGGAACC 384
                                                                  235 AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                     CTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTGTTACTGTGCGAGA-----
                                  CCAGGTAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGA---AGCACCAACTAC
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/259,372A
FILING DATE: 14-7UN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-APR-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/576,036
FILING DATE: 27-APR-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/576,036
APPLICATION NUMBER: US 07/538,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco COUNTRY: CA COUNTRY: USA ZIP: 9411-3834 COMPUTER: READABLE FORM: MEDIUM TYPE: The PC COMPUTER: TBM 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
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APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
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FILING DATE: 15-JUN-1990
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Patent No. 5565354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuvalThrvalSerSer 146
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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181 GGTAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTACAACCCG 240
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Patent No. 5648077

CENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaValProArgTrpValValSerGln 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
Length:
Matches:
Conservative:
Mismatches:
Indels:
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,372
APPLICATION NUMBER: 14-UIN-1994
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CURENT APPLICATION DATA.
APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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61 GIGCAGCTACAGCAGTGGGGGGGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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Mismatches:
Indels:
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FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-UNN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
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Best Local Similarity:
Query Match:
DB:
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Search completed: June 3, 2003, 09:47:23 Job time: 12.173 secs

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Ig kappa chain - human

[19 kappa chain - human
[2] kappa chain - human | kappa chain chai
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S41809
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K1HU12
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Percent Similarity:
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Alignment Scores:
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-MODEL=frame+ n2p.model -DEV=xlp
-Q=/CG12 1/USFTO spool/US08728463/runat 03062003 085615 16827/app query.fasta_1.3690
-DB=FIR 73 -QFMT=fastan -SUFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=Dits -START=1 -END=-1 -MATRIX=bloaum62 -TRANS=human40.cdi -LIST=45
-UNITS=Dits -START=1 -END=-1 -MATRIX=bloaum62 -TRANS=human40.cdi -LIST=65
-UNITS=Dits -START=1 -END=-1 -MATRIX=bloaum62 -TRANS=human40.cdi -LIST=65
-UOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-USR=US08728463 @CGN 1 1.77 @runat 03062013 085615 16827 -NCPU=6 -ICPU=3
-UNO MMAP -LARCEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                         protein search, using frame_plus_n2p model
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Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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Qy 121 GTCACCATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCAT 180 Db 41 ValThrIleThrCysArgalaSerGlnGlyIleSerSerTrpLeualaTrpTyrGlnGln 60 Qy 181 AAACCAGGGAAAGCCCCTAAGCTCTGTGTTTTGCAAAGTGGGGTC 240 Db 61 LysPrGGlyLysAlaBroLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal 80 Qy 241 CCATCAAGGTTCAGCGGCAGTGGACTGGGAGATTTCACTCTCACCATCAGCAGCTG 300 Db 81 ProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100 Qy 301 CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTTACCG 351 Db 101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnAlaAsnSerPhePro 117 RESULT 3 3	Ig kappa chain V-J region - human C'species: Homo sapiens (man) R'Atlain, R's Jaenhachen, R's Zachau, H'G. R'Atlain, R's Jaenhachen, R's Zachau, H'G. Bur. J. Immunol. 23, 3248-3271, 1993 A/Title: Expressed human immunoglobulin chi genes and their hypermutation. A/Reference number: 840312; MUID: 9408691; PMID: 8258341 A/Accession: 840333 A/Status: preliminary; translation not shown A/Molecule type: mRNA A/Rolecule type: mannoglobulin homology < IMM> A/Ingmment Scores: C's Superfamily: immunoglobulin homology < IMM> Alignment Scores: C's Score: Conservative: 10 Best Local Similarity: 88.00\$ Mannaches: 5 Best Local Similarity: 88.00\$	84.53* Indels: 2	21 133 41 193 61 253 81 313 101 101 121
	RESULT 2 S21527 Ig Kappa chain precursor V-I region - human (fragment) C; Species: Home sapiens (man) C; Species: Home sapiens (man) C; Species: Home sapiens (man) C; Date: 20-Feb-1995 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000 C; Accession: S11699; S34076; S3151; S2152; S. Mol. Biol. 183, 291-299, 1985 J. Mol. Biol. 183, 291-299, 1985 A; Atile: Alarge section of the gene locus encoding human immunoglobulin variable region A; Accession: S11699 A; Accession: S11699 A; Residues: 1-117 <-PEC. A;	A; Residues: 30-117 < WA2> A; Cross-references: BMBL:X66044; NID:g33320; PIDN:CAA46843.1; PID:g33321; EMBL:X66043; N A; Experimental source: patient 7 A; Accession: S34105 A; Molecule type: DNA A; Residues: 30-117 < WAG> A; Rosidues: 30-117 < WAG> A; Cross-references: EMBL:X66044; NID:g33320; PIDN:CAA46843.1; PID:g33321 A; Experimental source: patient 8 A; Introns: 19/1 C; Superfamily: immunoglobulin V region: immunoglobulin homology.	C;Keywords: heterotetramer; immunoglobulin F;38-112/Domain: immunoglobulin homology <imm> Alignment Scores: 8.49e-45</imm>

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C,Keywords: heterotetramer; immunoglobulin F;31-105/Domain: immunoglobulin homology <IMM>
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                           Ig Kappa chain - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 66-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40334
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3246-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Reference number: S40313
A;Reference number: S40314
A;Residues: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-132 <KLEs
A;Cross-references: EMBL:X72444
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <INMs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 TCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 CysAspIleGlnLeuThrGlnSerProSerPheLeuSerAlaSerIleGlyAspArgVal.40
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (cispecies: G-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 Cisacession: $40316
Cispecies: Accession: $40316
Riklain, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACATGATGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTCTGGTTCCCCAGGTTCCAGA
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A, Status: preliminary; translation not shown
A; Molecule type: mRNA
A; Residues: 1-125 «KLL»
A; Cross-references: EMBL:X72426
C; Superfamily: immunoglobulin V region; immunoglobulin homology
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81 GlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheAlaIle 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 GlnSerProSerSerValSerAlaSerValGlyAspArgValThrIleThrCySArgAla 40
                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                  CAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LeuLeulleTyrHisIleSerSerLeuGlnThrGlyValProSerArgPheSerGlySer
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R;Klein, R.; Jaenichen, R.; Zachau, H.G.
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
A;Ur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; WUID:94080891; PMID:8258341
A;Accession: $40369
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A;Residues: 1-129 «KLE»
A;Cross-references: EMBL:X72479; NID:g441426; PIDN:CAA51147.1; PID:g441427
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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64 TGCGACATC	Pred. No.: 7.71e-43 Length: 117

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Gispecies: Homo sapiens (man)
Cispecies: Homo sapiens
Cispecies: Cispe
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                                                                                                                                  21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg
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C;Species: Homo sapiens (man)
C;Accession: 552793
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995
A;Reference number: S52789
A;Reference number: S52789
A;Reference number: S52789
A;Residues: preliminary
A;Residues: 1-129 <ROC>
A;Residues: 1-129 <ROC>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
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                                               A;Cross-references: EMBL:X72477 C;Superfamily: immunoglobulin homology C;Superfamily: immunoglobulin v region; immunoglobulin homology C;Keywords: heteroterramer; immunoglobulin P;33-107/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-127 < KTJ
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Species: Homo sapiens (man)
Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 21-Jan-2000
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                                                                                                                                                                                                            'Species: Homo sapiens (man)
|Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
|Accession: S40331
                                                                                                                                                                                                                       C;Date: 06-Mar:1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C;Accession: $4031
R;Klein, R.; Jaenfuchen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: S40331
A;Accession: Status, A;MID:94080891; PMID:8258341
A;Accession: S40331
A;Accession: S40331
A;Catus: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 AKLES.
A;Molecule type: mRNA
A;Cross-references: EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PID:9441351
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>
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A)Comparation: 2p12-2p12
A.Map position: 2p12-2p12
A.Map position: 2p12-2p12
A.Map position: 2p12-2p12
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kai hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into 1) C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin V region (Walker) #status predicted (*Mar)
F.13-12/Domain: signal sequence #status predicted (*Mar)
F.23-12/Pomain: immunoglobulin homology < IMM>
F.33-112/Domain: immunoglobulin homology < IMM>
F.46-56/Region: complementarity-determining 1
F.57-71/Region: complementarity-determining 2
F.57-71/Region: complementarity-determining 2
                                                                                                                                              human lymphoid cell
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C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 2
C;Accession: A01883
R;Klobeck, H.G;; Combriato, G; Zachau, H.G.
Nucleic Acids Res. 12, 6995-7006, 1984
A;Title: Immunoglobulin genes of the kappa light chain type from A;Reference number: A93534; MUID:85014148; PMID:6091049
A;Recession: A01883
A;Molecule type: DNA
A;Residues: 1-129 <KLO>
A;Note: the sequence was determined from the differentiated gene C;Genetics:
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C;Species: Homo sapiens (man)
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F:111-119/Region: complementarity-determining
F:120-129/Region: framework 4
F:45-110/Disulfide bonds: #status predicted
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CGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGGAAAGCC 195
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C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000 C;Accession: A49134; S25115 R;Rocca, A.; Khamlichi, A.A.; Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, J.I. Clin. Exp. Immunol, 91, 506-509, 1993 A;Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in light A;Reference number: A49134; MUID:93185310; PMID:7680298
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Cibate: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
Cibate: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
Ciraccession: $4034 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
Riklein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080991; PMID:8258341
                                                                                                            A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-141 <ROC>
A;Residues: 1-141 <ROC>
A;Cross-references: EMBL:K67322; NID:g33268; PIDN:CAA47736.1; PID:g33269
A;Note: sequence extracted from NCBI backbone (NCBIP:127088)
C;Superfamily: immunoglobulin y region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>
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A;Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;33-107/Domain: immunoglobulin homology <IMM>

A:Status: preliminary; translation not shown

A; Residues: 1-125 <KLE> A; Molecule type: mRNA

315

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MEDLINE-81098966; PubMed-6779204;
Bentley D.L., Rabbitts T.H.;
"Human immunoglobulin variable region genes -- DNA sequences of two V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                 COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
                                                                             F941FA07D4AFC2F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-I region HK102 precursor (Fragment).
Homo sapiens (Human).
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Matches:
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                                               SIMILARITY
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Nature 288:730-733(1980)
                                                             129
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=81098966; Pubmed=6779204;
Bentley D.L., Rabbitts T.H.;
"Human immunoglobulin variable region genes -- DNA sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAPPA CHAIN V-I REGION HK102.
                                                                                                                                                                            COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                        COMPLEMENTARITY - DETERMINING - 2
                                                                                                                                                                                                                                   COMPLEMENTARITY - DETERMINING - 3
                                                                                                                                                                                                                                                                           12768 MW; ADIDF3A40AF1A49B CRC64;
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102
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region HK101 precursor (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
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FRAMEWORK-
                                                 Genew; HGNC:5741; IGKV1-5.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
EMBL; J00245; AAA59087.1; -. EMBL; Z00001; CAA77292.1; -. PIR; A01882; KIHU12. HSSP; P01607; IREI.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-85014148; PubMed-6091049;
Klobeck H.G., Combriato G., Zachau H.G.;
Immunoglobulin genes of the kappa light chain type from two human
lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-UU-1999 (Rel. 38, Last annotation update)
15-UU-1999 (Rel. 38, Last annotation update)
16 kappa chain V. I region Daudi precursor.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG KAPPA CHAIN V-I REGION DAUDI.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerTyrPro
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FRAMEWORK-3.
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PIR; A01884; KIHUDI.
HSSP; P80362; 1WTL.
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InterPro; IPR003596; Ig_V.
InterPro; IPR003596; Ig_V.
SWART; SMO0406; IGV; 1.
Immunoglobulin V region; Signal.
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P04432;
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                                                                                        MEDLINE=83129397; PubMed=6402305;
Bentley D.L., Rabbitts T.H.;
"Evolution of immunoglobulin V genes: evidence indicating that
recently duplicated human V kappa sequences have diverged by gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCG 351
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTAR. TY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
STGNAL
  kappa genes and a pseudogene.";
Nature 288:730-733(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12799 MW;
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InterPro; IPR003596; 1g v.
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PIR, A21056, A21056.
HSSP, P01607, 1REI.
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                                                                                                                                                                 GAAGATITIGCAACTIACTATIGICAACAGGCTAATAGTITICCCGTACACTITIGGCCAG 366
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                                                              ArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro
                                               GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGGTCCCATCA
                                                                                                         AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-81052342; PubMed-6776411;
Altenburger W., Steinmetz M., Zachau H.G.;
"Functional and non-functional joining in immunoglobulin light chain
                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 01, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 Kappa chain V.V region Tl precursor.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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FRAMEWORK-1.
COMPLENENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
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| 101 GlyThrThrValAspijeLys 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P80362; 1WTL.
InterPro; IPR003006; 19_MHC.
InterPro; IPR003596; 19_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes of a mouse myeloma.";
Nature 287:603-607(1980).
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473.00
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P01637;
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THOUSELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

BR PIR; A01877; KIHUMS.

BR PIR; A01877; KIHUMS.

BR INTERPRO; IPR003506; IG MHC.

BR INTERPRO; IPR003506; IG MHC.

BR RIMERPRO; IPR0047; IG's 1.

BR SMARY; SW00406; IG's 1.

FT DOWAIN 24 SOWDLEMBEYTARITY-DETERMINING-1.

FT DOWAIN 35 49 FRAMEWORK-2.

FT DOWAIN 50 56 COMPLEMBEYTARITY-DETERMINING-2.

FT DOWAIN 57 88 FRAMEWORK-3.
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                                                                                                                           CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTT
       AAACCAGGGAAAGCCCCTAAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                      GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Wes.
19 homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein lure of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=81092279; PubMed=6778806; Kratzin H., Yang C., Krusche J.U., Hilschmann N.; Kratzin H., Yang C., Krusche J.U., Hilschmann N.; Preparative separation of the tryptic hydrolysate of a protei high-pressure liquid chromatography. The primary structure of monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    782B14A649A60E45 CRC64;
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Query Match:
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P01611;
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KV1S_HUMAN
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                                                                       67 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCAC 126
                                                                                                1 AspileGinMetThrGinSerProSerThrLeuSerAlaSerValGiyAspArgValAla 20
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                                                                                                                                                                                             21 IleThrCysArgAlaSerGlnAsnIleSerSerTrpLeuAlaTrpTyrGlnGlnLysPro
                                                                                                                                                                                                                                                                                         41 GlyLysAlaProLysValLeuIleTyrLysSerSerSerLeuGluSerGlyValProSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal kappa-type immunoglobulin I
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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R PIR; A01868; KIHUHU.

R HSSP; P80362; 1MTL.

DR HIGEPTO; IPRO0306; Ig_W.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGV; 1.

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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
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-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Homo sapiens (Human)
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                        US-08-728-463B-206 (1-388) x KV1D_HUMAN (1-107)
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34 CO
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97 CO
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11671 MW;
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-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.";
Eur. J. Biochem. 49:377-391(1974).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
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"Primary structure of kappa light chain from a human myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E1BF0DF9844C3346 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region CAR.
Homo Sapiens (Human).
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                                                                  US-08-728-463B-206 (1-388) x KV5E_MOUSE (1-128)
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467.50
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P80362; 1WTL.
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Query Match: DB:

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127 ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 186
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                              1 AspileGinLeuThrGinSerProSerSerLeuSerMasSerValGiyAspArgValThr
                                                                            21 IleThrCysArgAlaSerGlnSerValTyrAsnTyrValAlaTrpPheGlnGlnLysPro
                                                                                                            187 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA
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"The primary structure of the Bence-Jones protein Kue. The amino acid
sequence of the variable part of a human L-chain of the kappa-type.";
HOPPE-Seyler's Z. Physiol. Chem. 360:725-734(1979)
-I- MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-I- MISCELLANBOUS: THE IS A BENCE-JONES PROTEIN.
PIR; A01870; KIHUKU.
HSSP; P01607; IREI.
InterPro; IPR003066; Ig MHC.
InterPro; IPR003066; Ig W.
Pfam; PP00047; ig; I.
SMART; SM00406; IGv; I.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo..
NCBI_TaxID=9606;
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COMPLEMENTARITY-DETERMINING-1.
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FRAMEWORK-3.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Kue.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Dwulet F.E., O'Connor T.P., Benson M.D.;
Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
MO1 Immunol. 23.73-78 (1996).
PIR, AOL878; KIHUBN.
PIRS, P80362; 1WTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Efam; PF00047; ig; 1.
SWART; SM00406; IGV; 1.
Immunoglobulin V region; Amyloid.
DOMAIN.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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FRAMEWORK-4.
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13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Homo sapiens (Human).
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Palm W., Hilschmann N.;
"The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein, a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ArgPhelleGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=76039968; PubMed=1182131;
Epp O., Lattman B.E., Schiffer M., Huber R., Palm W.;
"The molecular structure of a dimer composed of the variable po of the Bence-Jones protein Refired at 2.0-A resolution.";
Blochemistry 14:4943-4952(1975).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
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PIR, A01873; KIHURE.
PDI; 1RF1; 17-FEB-84.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGy: 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
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Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975)
                     Conservative:
Mismatches:
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Rei.
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A Gall W.E., Edelman G.M.;

The covalent structure a human gamma G-immunoglobulin. X.

Intrachain disulfide bonds.";

Intrachain disulfide bonds.";

Biochemistry 9:3188-3196(1970).

-! MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-! MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE STRUM PROTEIN.

R PIR, A01866; KIHUEU.

R PIR, 101607; 1REI.

R InterPro; IPR003006; Ig MHC.

R InterPro; IPR003596; Ig MHC.

R Fam; PR0047; ig; 1.

R SMART; SM00406; IGy, 1.

M Immunoglobulin V region.
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Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VI. Amino
acid sequence of the light chain.";
Biochemistry 9:3155-3161(1970).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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COMPLEMENTARITY-DETERMINING-3.
FRAMENORK-4.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-I region EU.
Homo sapiens (Human).
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67 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 126
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                                                        MEDLINE=83273707; PubMed=6410398;
MEDLINE=83273707; PubMed=6410398;
Goni F., Frangione B.;
Goni F., Frangione F., Frangione B.;
Frangione B., Frangione B.;
Goni F., Frangione F., Frangione B.;
Goni F., Francis G.;
Goni F., Francis 
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HSRS, P80622; 1WTL.
HSRSP; P806262; 1WTL.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
COMPLEMENTARITY-DETERMINING-1.
COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
    Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 30, Last annotation update)
19 kappa chain V-I region GAL.
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                           COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
   COMPLEMENTARITY-DETERMINING-1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V.I region WEA.
Homo sapiens (Human).
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81 GluAspileAlaThrTyrTyrCysGlnGlnTyrAspTyrLeuProTrpThrPheGlyGln 100 . ∂

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Search completed: June 3, 2003, 09:04:03 Job time: 9.35964 secs

(Human)

sapiens

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     Eukaryota, Merazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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FRAMEWORK-4.
BY SIMILARITY.
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HSSP, P01607; IREI.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; ig, 1.
SWART; SM00406; IGV; 1.
Immunoglobulin V region.
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Best Local Similarity:
Query Match:
DB:
                     NCBI_TaxID=9606;
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KV1B_HUMAN
ID_KV1B_HUMAN
AC_P01594;
DT_21-JUL-1986
DT_21-JUL-1986
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67 GACATCCAGATGACCCAGTCTCCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 126
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1- MISCELLANGOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF THE KAPPA CHAIN REI.

1- MISCELLANGOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

1- MISCELLANGOUS: THIS IS A BENCE-JONES PROTEIN.

PIR, A01862, KLHUBU.

HSSP, P01607, IREI.
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Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
protein Au).";
                                                        Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                    MEDLINE=77022433; PubMed=1234024;
Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E. Schwager P., Steigemann W., Schramm H.J.;
"The structure determination of the variable portion of the
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Matches:
Conservative:
Mismatches:
Indels:
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region AU.
Homo sapiens (Human).
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21-JUL-1986 21-JUL-1986

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0920e9 mus musculu
090186 homo sapien
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AR035037; AAD56273.1; -.
INTESP: POLGO7; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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-Q=/Cgn2_1/USPTO_spool/US08728463/runat_03062003_085614_16815/app_query.fasta_1.3690
-Q=/Cgn2_1/USPTO_spool/US08728463/runat_03062003_085614_16815/app_query.fasta_1.3690
-UB-SENTERBEL_2.1 -QFMPH=fastan -SUPFIX=rspt -MINMATCH=b.1 -LOOPCL=0
-USPTS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -TRR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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187 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246
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                                                                                                                 67 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC
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A Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
A Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Tadecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin T antibody V region genes.";
J. Immunol. 16:12020-2031(1998).
R. EMBL; U96396; AAB68785.1; -
R. InterPro; IPR003006; Ig_MHC.
R. Pfan; PF00047; ig; 1.
T. NON TER 107 107
TONN TER 107 107
C SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fregment).
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Q96SA9;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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BEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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Clin. Immunol. Immunopathol. 87:184-192(1998).
BMB.; AF035040, 1REI.
HSSP; PO1607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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108 AA; 11738 MW;
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SWART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

TISSUB-COLON;
Straubberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC015292; AAH15292.1; -.
InterPro; IPR0013006; Ig MHC.
InterPro; IPR001865; Ribosomal_S2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 234 AA; 25929 MW; BODOBOEGEB7812D2 CRC64;
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90
115
0
0
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.9 kPa protein.
Mus musculus (Mouse).
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                PRT;
                                                   387
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                                                                       GlyThrLysLeuGluIleLys
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463.00
82.68%
70.87%
66.33%
                                                                                                                                                PRELIMINARY;
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Best Local Similarity:
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                                                                                                                RESULT 5
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                                                                               GGGAAAGCCCCTAAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246
                                                                                                                                             247 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 306
                                                                                                                                                                                                            GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366
                                    21 IleThrCysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnLysPro 40
                                                                                                 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
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                   ATCACTTGTCGGCCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUB=COLON;
Straubberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027418; AAH27418.1;
Hypothetical protein.
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234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64
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92
113
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25,9 kDa protein.
Mus musculus (Mouse).
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Matches:
Conservative:
Mismatches:
Indels:
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470.00
82.68%
72.44%
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Query Match:
DB:
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Pred. No.:
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27 ATCACTIGICGGGCGGGCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 GACATCCAGATGACCCCAGTCTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC
                                                  Euteleostomi;
                                                                                              SEQUENCE FROM N.A.
MEDLINE=89277139; Pubmed=9614934;
ML X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.,
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo'sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                        nomo appreme vaumani.
Eukaryota, Metazoma Chordata, Craniata, Vertebrata, Butel.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                   DB5845F19724FB4E CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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EMBL, AF035035; AAD56271.1; -
HSSP, PO1607; IREI.
InterPro; IPR003006; Ig WHC.
InterPro; IPR003596; Ig_v.
Pfam; PR00047; ig; 1.
NON_TER.
InterPro; IPR00406; IGv.
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SEQUENCE 108 AA; 11787 MW;
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456.00
89.72%
84.11%
65.33%
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                                Homo sapiens (Human)
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Best Local Similarity:
Query Match:
DB:
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SEQUENCE FROM N.A.
                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                  Fetus.";
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DT 01-M2
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|GluAspPheGlySerTyrTyrCysGlnHisHisSerGlyIleProPheThrPheGlySer 120
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                   Straubberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC019474; AAH19474.1; ...
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
R InterPro; IPR003596; Ig_V.
R SMART; SM00407; IG; 2.
SMART; SM00409; IG; 2.
R SMART; SM00406; IG_MHC; UNKNOWN_1.
R PROSITE; PS00299; IG_MHC; UNKNOWN_1.
Hypothetical protein.
W Hypothetical protein.
SEQUENCE 234 AA; 25702 MW; 10255IC58AC2FA9F CRC64;
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87
18
22
0
                      01-MAR-2002 (TYEMBLrel. 20, Created)
01-MAR-2002 (TYEMBLrel. 20, Last sequence update)
01-UJN-2002 (TYEMBLrel. 21, Last annotation update)
Hypothetical 25.7 kDa protein.
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Last sequence update)
Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
  234 AA
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AC Q9UL79;
DI 01-MAY-2000 (TEMBLrel. 13, C
DT 01-MAY-2000 (TEMBLrel. 13, 1
DT 01-DEC-2001 (TEMBLrel. 19, 1
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462.00
82.68%
68.50%
 PRELIMINARY;
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                           TISSUE=COLON;
                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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Q9UL79
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us-08-728-463b-206.rspt

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Wilde K.G., Yu.X., Ekramoddoullah A.K.M., Misra S.;

T. "Cloning of CDNAs encoding for anti-white pine blister rust monoclonal

XT antibody (Mab 7, its light and heavy chains) and construction of a

S. Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

R. Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

R. RENBL, AFI52371; AAA40242.1; -..

R. RSP; PO1679; ZFBJ.

R. TREAPRO; PR003606; Ig MHC.

DR FRAM; SM00410; IG Jike; 1.

DR SMART; SM00410; IG Jike; 1.

DR ROWSITE; PS00290; IG MHC; UNKNOWN_1.
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                                                                                                                                                                                                                  GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366
                                                                                                                                                                                                                                         PhelleCysGlnAlaSerGlnAspIleAlaAsnHisLeuAsnTrpTyrGlnLysLysPro 40
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                                           GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA
                                                                 Mus muscúlus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Conservative:
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                                                                                                                                                                                                                                                                                                        367 GGGACCAAGCTGGAGATCAAA 387
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GlyThrLysValAspPheLys 107
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23922 MW;
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402.00
85.05%
70.09%
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214 AA;
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Best Local Similarity:
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0981A5
1D 01-MA
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                                                                                                                              10 LeuLeuLeuCysPheGlnGlySerArgCysAspIleGlnMetThrGlnThrThrSerSer 29
                                                                                                                                                                                                                       30 LeuSerAlaSerLeuGlyAspArgValThrIleSerCysSerGlySerGlnGlyIleAla 49
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                                                                                                          CTGCTGCTCTGGTTCCCAGGTTCCAGATGCGACATCCAGATGACCCAGTCTCCATCTTCC
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MEDLINE=21361171; PubMed=11468171;
COMENZO R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
"The tropism of organ involvement in primary systemic amyloidosis: contributions of Ig V(L) germ line gene use and clonal plasma cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 GCTAATAGTTTCCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA 387
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Kappa 1 light chain variable region (Fragment).
SDNK1.
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                                                               US-08-728-463B-206 (1-388) x Q91WS9 (1-233)
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Blood 98:714-720(2001).
Blood 98:714-720(2001).
EMBL; AF9161758; AAK51465.1; -.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
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116 AA; 12735 MW;
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414.00
85.05%
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59.31%
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  Query Match:
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Q96PF6
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Alignment Scores
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MEDLINE=99306687; PubMed=10380019;
Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
Foon K.A., Chatterjee S.K.;
"Construction and characterization of a chimeric fusion protein
consisting of an anti-idiotype antibody minicking a breast cancer-
Hybridoma 18:193-202(1999).
EMBL; AF124721; AAK55120.1;
                                                                    Myosin-reactive autoantibodies in rheumatic carditis and normal
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Mus musculus (Mouse).

Mukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus
MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
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107 AA; 11501 MW; 070549FDE0754748 CRC64;
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89
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Immunoglobulin light chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                     fetus.",
Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035033; AAD56269.1; -
HSSP; PO1607; IREI.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
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89.72%
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Best Local Similarity:
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NON TER
SEQUENCE
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67 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 126
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| IOI GludspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mush.
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. InterPro; IPR003006; Ig_MHC.

Pfam, PF00047; igj, 2.

PROSITE; PS002290; IG_MHC; UNKNOWN_1.
                                                         13F61BEBBB981FAS CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
10-DAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.8 kba protein (Fragment).
                                                                                                         Length:
Matches:
Conservative:
Mismatches:
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Pfam; PF00047; ig; 1.
NON_TER 127 127
SEQUENCE 127 AA; 13794 MW;
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                                                                                                     3.69e-41
439.00
77.95%
69.29%
62.89%
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Best Local Similarity:
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Best Local Similarity:
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us-08-728-463b-206.rspt

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295 AGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTAC 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 CAGCATAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGT 234
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                        STRAIN=BALB/C; TISSUE=SPLEEN;
MEDLINE=20183931; PubMed=10706631;
Shinohara N., Demura T., Fukuda H.;
"Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction
                                                                                                                                                                                                                                                                    E0F96B8A17004317 CRC64;
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Matches:
Conservative:
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Indels:
Gaps:
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EMBL, AB03631, BAA88633.1; -.
HSSP, P01607, IREI.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
Ffam, PR00047; Ig; 2.
SMART, SMO0406; IGv; 2.
SEQUENCE 298 AA; 31867 MW; E0F96BBA17004317 (
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01-MAY-2000 (TrEMBLrel
01-DEC-2001 (TrEMBLrel
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Mus musculus (Mouse).
                                                                                                                    (Fragment).
Mus musculus (Mouse)
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                                            127 ATCACTIGICGGGGGGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 186
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.,
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                         01-MXY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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EMBL; AF035031; AAD56267.1; -.
HSSP; P80362; IWTL.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
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394.00
85.98%
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Best Local Similarity:
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                                                                                                                                                                                                                                                              Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
"Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells.",
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF307938; AAL09422.1;
InterPro; IPR003006; Ig_MHC.
Pfam. PF00047; ig; 1.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
prerin-mimicking anti-idiotope kappa chain variable region
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Human protein sequ
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SUMMARIES
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AAW70379
AAY96289
AAY96301
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ABG18767
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AAY56723
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-Q=/cgn2_1/USPTO spool/US08728463/runat_03062003_085613_16797/app_query.fasta_1.3690

-Q=/cgn2_1/USPTO spool/US08728463/runat_03062003_085613_16797/app_query.fasta_1.3690

-DB=A Geneseq_101002 - OFMT=Esatan - SUFFTX=rag - MINNATCH=0.1 - LTOOPCiL=0

-LOOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi

-LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15

-MODE=LOCAL - OUTFMT=pto - NORM=ext - HEAPSIZE=500 - MINLEN=0 - MAXLEN=200000000

-USRENG08728463 GCGR 1 1 333 Grunat 0 3085613 16797 - NOPU=6 - ICPU=3

-NO MMAP - LARGEQUERY - NEG_SCORES=0 - WAIT - DSPELOCK=100 - LONGLOG

-DEV_TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPDP=10 - XGAPEXT=0.5 - FGAPOP=6

-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
                                                                                                            3, 2003, 08:56:21 ; Search time 25.0964 Seconds (without alignments) 4120.219 Million cell updates/sec
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1 ATGCACATGATGGTCCCCGC......GACCAAGCTGGAGATCAAAC 388
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Copyright (c) 1993 - 2003 Compugen Ltd
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Listing first 45 summaries
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The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomedulatory molecule (AILIM). (I) is useful for modulating signal transduction into a cell mediated by AILIM, for modulating spoiliferation of AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity adiants AILIM-expressing cells and/or immune cytolysis or apoptosis of prophylaxis of delayed type allergy. (I) is useful for treating and preventing various diseases associated with AILIM-mediated costimulatory transduction, and for inhibiting the onset and/or prevention and/or treatment of rheumatoid arthritis, multiple to advancement of the diseases. (I) is useful for suppression, prevention and/or treatment of rheumatoid arthritis, multiple collinamatory dermatosis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, psoriasis, autoimmune thyroiditis, speriasis, autoimmune thyroiditis, speriasis, autoimmune diabetes mellitus, psoriasis, autoimmune con allergic disorders, inflammation, graft versus host reaction, graft versus host immunity, specifically inflammatory intestinal disorders such as ulcerative collitis, pneumonia, hepatitis, nephritis, vasculitis, and collitis, pneumonia, immune, i.e., human anti-mouse antigenicity (HAMA) in a host.

ANU74296-ANU74296-ANU74301 represent antigenicity (MAU74296-ANU74301 represented antigenicity and programmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human monoclonal antibody that binds to activation inducible
lymphocyte immunomodulatory molecule, useful for treating rheumatoid
arthritis, multiple sclerosis and inflammation
ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 30; Page 270-271; 300pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             Hori N;
                                                                                                                                                                                                                  15-MAY-2001; 2001WO-JP04035
                                                                                                                                                                                                                                                                    18-MAY-2000; 2000JP-0147116.
30-MAR-2001; 2001JP-0099508.
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                                                          Homo sapiens.
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Length: Matches: Conservative: Mismatches: Indels: Gaps: 3.27e-56 624.00 95.35% 93.80% 89.40% Percent Similarity: Best Local Similarity: Sequence 236 AA; Alignment Scores: Query Match: DB:

236 121 2 6 0

US-08-728-463B-206 (1-388) x AAU74297

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CCATCAAGGTTCAGCGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 300 100 41 ValThrileThrCysArgAlaSerGlnGlyIleSerArgLeuLeuAlaTrpTyrGlnGln 60 80 181 AAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC 61 LysProGlyLysAlaProLysLeuLeuIleTyrValAlaSerSerLeuGlnSerGlyVval CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTT Immune response protein, HIRP1; human, immunological disease, cell proliferation, cancer; anti-HIV; antiallergic, antiatedic; antiasthmatic; antiatedicordistic, antipsoriatic; immunosuppressive; dermacological; antidiabetic; antinflammatory; neuroprotective; osteopathic; antirheumatic; antiarthritic; antiulcer; virundide; antibacterial; fundicide; protozoacide; antholamintic; vulnerary; hepatotropic; cytostatic; therapy; diagnosis; vaccine; immunoglobulin. 'note= "immunoglobulin kappa complex motif" 98. 134 /note= "T-cell glycoprotein CD8 motif" note= "immunoglobulin domain motif" "immunoglobulin domain motif" note= "O-phosphorylated" note= "O-phosphorylated" note= "O-phosphorylated" note= "O-phosphorylated" /note= "O-phosphorylated" 209 361 GGCCAGGGACCAAGCTGGAGATCAAA 387 note= "O-phosphorylated" note= "O-phosphorylated" note= "O-phosphorylated" note= "O-phosphorylated" 2..241 |abel= Mature_protein 'label= Signal_peptide response protein HIRP1. AAB82912 standard; Protein; 241 AA. Location/Qualifiers (first entry) .223 23..240 38..117 note= Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Human immune 26-NOV-2001 Homo sapiens, 121 AAB82912; 241 301 Peptide Protein Domain Region Region Domain Region Key AAB82912 ò g ð 셤 ò 셤 ò

19..225 note= "Ig MHC motif" 197..240 Region

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The sequence represents the variable light chain segment of a human monoclonal antibody (HuMAb) against interleukin-1-alpha. The MAb is of subclass 1964 and binds to lymphokines/monokines with an affinity of 10(9)/M. The Mab or fragment (FV, single-chain FV, Fab or F(ab') 2) is used in the treatment of inflammation e.g. rheumatoid arthritis, osteoarthritis and inflammatory bowel diseases, and in the treatment of psoriasis, allergy, septic shock, graft vs host disease and tumours. The MAb or fragment can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Cynomologous Vkappa cDNA clone 4-10.
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                                                                                                                                                                                    The invention provides an antibody (Ab) comprising donor CDRs (complementarity determining regions) derived from a non-human antigenspecific donor antibody, and an acceptor framework from a non-human primate. The Abs are prepared by grafting CDRs from a non-human matigenspecific donor antibody onto homologous Old World ape or monkey acceptor frameworks. The Abs have reduced immunogenicity and are better tolerated in humans (because of the close similarity between the human and primate proteins), but retain the full antigen-binding affinity of the donor
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                                                                                    Antibodies containing donor complementarity determining regions and non-human primate acceptor frameworks, having reduced immunogenicity in
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61 AGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention is based on the discovery of new human immune response proteins (HIRP), the polynucleotides encoding them, and the use of these compositions for the diagnosis, treatment or the use of these compositions for the diagnosis, treatment or prevention of immunological and cell proliferative disorders.

The present sequence is that of human immune response protein 1 proportions of the present sequence is that of human immune response protein 1 polynucleotide assembled e.g. from a lung adenocarcinoma CDNA ibrary clone. The amino acid sequence shows homology from tesidue W123 to C241, to an HIV-1 antigen binding protein, and of urther homologies suggest that it may be an immunologilal from the diagnosis, curther homologies suggest that it may be an immunologilal polynucleotides and polypeptides are useful for the diagnosis, cancers, arretiosclerosis, actinic keratosis, bursitis, mixed connective tissue disease, actinic keratosis, poriasis, cancers, arretiosclerosis, actinic keratosis, poriasis, connective tissue disease (MCTD), myelofibrosis, poriasis, leukaemia, hepatitis, cirrhosis and atherosclerosis), and immunological disorders e.g. AIDS, Addison's disease, acutofmune diseases, contact dermatitis, diabetes mellitus, cholecystitis, multiple sclerosis, irritable bowel syndrome, osteoporosis, multiple sclerosis, irritable bowel syndrome, osteoporosis, rheumacoid arthritis, ulcerative colitis, trauma, and viral, antaonist connective also used to screen for agonist and antaonist connective colitis, incared and antaonist and antaonist connective colitis, incared and antaonist and antaonist and antaonist antaonist connective colitis, trauma, and viral, antaonist connective colitis, resented and disease.
                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human immune response proteins, for treating immunological disorders and cell proliferative disorders, and for assessing the effects of exogenous compounds on the expression of HIRP molecules
                158..180
/note= "immunoglobulin and MHC protein motif"
219..236
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                                                                                                                                                                                                                                                                                                                             Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 85; 95pp; English
                                                                                                                                                                                                                                           15-MAR-2000; 2000US-189417P.
                                                                                                                                                                                                 15-MAR-2001; 2001WO-US08518
                                                                                                                                                                                                                                                                                (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.23e-52
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91.79%
83.58%
84.46%
                                                                                                                                                                                                                                                                                                                        Tang YT, Hillman JL,
                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-590044/66.
N-PSDB; AAH26799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 AA;
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                                                                                                                 WO200168696-A1.
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                                                                                                                                                           20-SEP-2001.
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285
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                                                                                                               ThrileSerSerLeuglnProAspAspPheAlaThrTyrTyrCysGlnGlnTyrAsnAsn 120
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TTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTC
                                                                                                    ACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGT
                           GCCTGGTATCAGCATAAACCAGGGAAAGCCCCTAAAGCTCCTGATCTATGCTGCATCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human monoclonal antibody against a human cytokine - used to mfr. medicament to treat inflammation.
                                                                                                                                                                                                                                                  Anti-interleukin-1-alpha human monoclonal antibody VL segment.
                                                                                                                                       TTCCCGTACACTTTTGGCCAGGGACCAAGCTGGAGATCAAA 387
                                                                                                                                                 TYrProTrpThrPheGlyGlnGlyThrLysValGlulleLys 134
                                                                                                                                                                                                                                                                                                                                                       to +23)"
                                                                                                                                                                                                                                                                    Monoclonal antibody; interleukin-1-alpha; cytokine; antiinflammatory; prophylactic; therapeutic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    111..117
/note= "CDR 3 (+89 to +95)"
118..130
/note= "JK 4 (+96 to +108)"
                                                                                                                                                                                                                                                                                                                                                                       "CDR 1 (+24 to +34)"
                                                                                                                                                                                                                                                                                                                                                                                                          "CDR 2 (+50 to +56)"
                                                                                                                                                                                                                                                                                                                                                                                         'note= "FR 2 (+35 to +49)"
                                                                                                                                                                                                                                                                                                                                                                                                                             "FR 3 (+57 to +88)"
                                                                                                                                                                                                                                                                                                                                   'note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                           AAR75394 standard; Protein; 130 AA
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                                                                                                                                                                                                                                (first entry)
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/note=
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Peptide
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Peptide Protein

Domain Domain Domain

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241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 300
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                                                                                  61 LysProGlyLyssAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
                                                                   GTCACCATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCAT
                                                                                                                                AAACCAGGGAAAGCCCCTAAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-human CD23 5E8 monoclonal antibody; light chain variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-human CD23 5E8 monoclonal antibody light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human CD23; IgE; FceRii/CD23; gamma-1 constant region; gamma-3 constant region; allergy; inflammation; autoimmune disease; allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New anti-human CD23 monoclonal antibody - used for inhibiting IgE expression to treat or prevent allergic, inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "anti-human CD23 5E8 light chain variable
                                                                                                                                                                                                                                                                                                                                                    TTTGGCCAGGGACCAAGCTGGAGATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Signal peptide"
23..129
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/note= "C
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/note=
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N-PSDB; AAV33309.
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20-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGACATGATGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGTTCCCAGGTTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baughn MR;
Human; immunoglobulin; IGFAM-10; IGFAM; immune disorder; cancer;
infection; inflammation; haematopoiesis; AIDS; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gorgone GA,
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Matches:
Conservative:
Mismatches:
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Yang J;
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                                                                                            1..22
/label= signal_peptide
23..23/
/label= IGFAM-10
38..112
/label= Ig_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     haematopoietic cancer (such as leukaem
bacteria, viruses, fungi or parasites.
                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 85-86; 105pp; English
                                                                                                                                                                                              99US-0113635.
98US-0113635.
99US-0128194.
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578.50
92.31%
88.46%
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Lal P, Hillman JL,
                                                                                                                                                                                                                                                                                                                                                99WO-US27566
                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE PHARM INC.
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22-DEC-1998;
07-APR-1999;
                                                Homo sapiens
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Yue H, Lu DAM,

Sequence

Query Match:

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ArgCysAspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 AA
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                                                                                                                                WO200029583-A2
                                                                                                                                                                     19-NOV-1999;
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07-APR-1999;
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                                                                                                                                                  25-MAY-2000
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Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
        Protein
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                         Domain
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                                    The present sequence represents the light chain variable region of primate monoclonal antibody anti-human CD23 5E8. The invention provides primate monoclonal antibodies which specifically bind human CD23, the low affinity receptor for IGE (FCERI/CD23), and comprise either of a human gamma-1 or human gamma-3 constant region that binds not human FC gamma receptors and inhibits IGE expression. The monoclonal antibodies of the invention are claimed to be useful for inhibiting and autoimmune conditions e.g. allergic rhinitis conjunctivitis, autoimmune haemolytic anaemia, etc.
                                                                                                                                                                                                                                                                                               61 AGAIGCGACAICCAGAIGACCCAGICICCAITTICCGIGICTGCAICIGIAGGAGACAGA 120
                                                                                                                                                                                                                                                                                                                                      GICACCATCACTIGICGGCGAGICAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCAT 180
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                                                                                                                                                                                                                                                                                                            CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                        Human; immunoglobulin; IGFAM-1; IGFAM; immune disorder;
infection; inflammation; haematopoiesis; AIDS; allergy.
                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                          Length:
Matches:
                 Example 1; Pages 106-108; 146pp; English.
                                                                                                                                                                                                                                       US-08-728-463B-206 (1-388) x AAW70379 (1-129)
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/label= signal_peptide
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                                                                                                                                                                        3.45e-51
575.00
90.70%
86.05%
82.38%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-2000 (first entry)
  auto:immune conditions
                                                                                                                                            129 AA;
                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                            Sequence
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DB:
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90
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Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders
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Yang J;
                                                                                                              /label _ Ig_signature
                                                                                                                                                                193..236 ___/label= Ig_domain
                            38.112
/label=_Ig_domain
                                                               150..219 __
/label= Ig_domain
154..176
13..237
'label= IGFAM-1
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98US-0113635.
99US-0128194.
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Lal P, Hillman JL,
                                                                                                                                                                                                                                                                                    99WO-US27566
                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE PHARM INC.
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The present sequence is the human immunoglobulin superfamily protein in Information Informati

Alignment Scores:		
Pred. No.: 4.38e-51	Length: 237	
Score: 574.50		
Percent Similarity: 91.54%	tive.	
: >:	Mignatches	
•	Indels:	
DB: 21	Gaps: 1	
US-08-728-463B-206 (1-388) x AAY96289 (1-237)	6289 (1-237)	
Qy 1 ATGGACATGATGGTCCCCG	1 ATGGACATGATGGTCCCCGCTCAGCTCTGGGCTTCTTGCTGCTGCTGCTTCTTGGTTCCTA	

g qo	MetaspMetargvalProAlaGlnLeuGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuL
λ̈́o	61 AGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTCTGCATCTGTAGGAGACAGA 120
4	

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04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                      Alignment Scores:
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                                                                                                                      Sequence
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Peptide
                                                                                                                                                                               Query Match:
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No.:
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                                                                           ProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
                                                                                                   CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTC---CCGTACACT 357
GTCACCATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCAT 180
                                                                241 CCATCAAGGTTCAGCGCCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 300
                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders
        41 ValThrIleThrCysArgAlaGlyGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGln
                                          LysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal
                                 AAACCAGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the human immunoglobulin superfamily protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baughn MR;
                                                                                                                                                                                                                                                           Human; immunoglobulin; IGFAM-13; IGFAM; immune disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gorgone GA,
                                                                                                                                                                                                                                                                     infection; inflammation; haematopoiesis; AIDS; allergy
                                                                                                                                              TTTGGCCAGGGACCAAGCTGGAGATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guegler KJ,
Yang J;
                                                                                                                                                                                                                                                                                                             1..22
/label= signal_peptide
23..23..23
/label= IGFAM-13
38..112
/label= Ig_domain
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                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                               150..219
/label= Ig_domain
193..236
/label= Ig_domain
                                                                                                                                                                                        AAY96301 standard; protein; 237
                                                                                                                                                                                                                                           Human IGFAM-13 immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0113635.
98US-0113635.
99US-0128194.
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Lal P, Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US27566
                                                                                                                                                                                                                          16-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-387796/33.
N-PSDB; AAA27393.
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22-DEC-1998;
07-APR-1999;
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                                                                                                                                                                                                                                                                                     Homo sapiens
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121
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Lu DAM,
                                                                                                                                                                                                                                                                                                            Peptide
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IGPAM-13. Its gene was isolated from a cDNA library of lung tumour tissue. It is expressed in reproductive, gastrointestinal and cardiovascular tissue, where cancer and inflammantion are common. The gene, protein, its antibodies, agonists and antagonists are suitable for disgnosing and treating many diseases, including cancer, immune, system disorders (such as inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's arteriosclerosis, pasoriasis, rheumatoid arteriose, especially systemic lupus erythemacrosus and ulcerative colitis, soleroderma, systemic lupus erythemacrosus and ulcerative colitis, complications of cancer, haemodialysis and extracorporeal circulation, trauma and haemacropoletic cancer (such as leukaemia) and infections caused by bacteria, viruses, fungi or parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ValThrMetThrCysArgAlaSerGlnSerIleSerThrTyrLeuAsnTrpTyrGlnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 ProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCT - - - AATAGTTTCCCGTACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGGACATGATGGTCCCCGCTCAGCTCCTGGGCTCCTGCTCTTGGTTCCCAGGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LysProGlyLysAlaProLysLeuLeulleTyrAlaAlaSerSerLeuGlnSerGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal antibody ZM1-2 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237
1112
9
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Matches:
Conservative:
Mismatches:
Indels:
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/label= leader_sequence
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574.50
93.08%
86.15%
82.31%
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                                                                                                                                                                                                                                                                                                                                                                                                       237 AA;
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Best Local Similarity:
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258
                                                                259 AGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCA 318
                                                                              378
                                                                                                                                                                                                                                                                                     Heavy chain; light chain; variable region; human; monoclonal antibody; immunisation; hepatitis B virus; HBV; vaccine; mouse; fusion; xenogeneic; peripheral blood lymphocyte; surface antigen; cell culture; ion exchange; chromatography; size separation; primer; PCR; polymerase chain reaction; amplification; hybridoma; infection; immunosuppression; hepatitis;
                                                                                                                     105 ThrTyrTyrCysGlnGlnAlaAspSerLeuProPheThrPheGlyGlyThrLysVal 124
       45 AlaSerGlnGlyIleSerSerTrpLeuAlaTrpTyrGlnGlnLyaProGlyLysAlaPro 64
                                                  84
                                                                                                       319 ACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAGGGGACCAAGCTG
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/note= "complementarity determining region
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/note= "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "complementarity determining region 116..128
                                                                                                                                                                                                                                                                                                                                                                                                   'note= "leader sequence"
                                                                                                                                                                                                                                                                                                                                                                                                             21..128
/note= "mature protein"
                                                                                                                                                                                                                                                                    Monoclonal antibody ZM1-2 Vl region.
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                        AAW24990 standard; Protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                21..115
/note= "VkI region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Jx region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-0871426.
86US-0904517.
88US-0192754.
90US-0538796.
91US-0676036.
94US-0259372.
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                                                                                                                                                                                                                                                 (first entry)
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|125 AspPheLys 127
                                                                                                                                              GAGATCAAA 387
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                                                                                                                                                                                                                                                                                                                                          liver transplant
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                                                                                                                                                                                                                                                 08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1997.
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27-MAR-1991;
14-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5648077-A.
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31-OCT-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-1988
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                           199
                                                                                    85
                                                                                                                                               379
                                                                                                                                                                                                                              AAW24990;
                                                                                                                                                                                                                                                                                                                                                                                Key
Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTCAGCTCCTGGGGCTCCTGCTGCTCTGGTTCCCAGGTTCCAGATGCGACATCCAGATG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44
                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibodies effective for the diagnosis and treatment of diseases caused by infection with hepatitis B have been prepared from cell line obtained by fusing a xenogenetc hybridoma designated SPAZ 4 with blood cells of a patient immunised with hepatitis B vaccine. Specific antibodies are PEI-1, ZMI-1, ZMI-2, MD3-4 and L03-3, each of these being of the 1gG1 class. The present sequence is the light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human monoclonal antibodies specific for hepatitis B surface antigen - are used to treat or prevent infection or in diagnostic assays
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109
7
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Matches:
Conservative:
Mismatches:
 21..115
/label= V_kappa_I_region
                      21..43
/label= framework_region
                                        44..54
/label= CDR1
55..69
/label= framework_region
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                                                                                                            framework_region
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                                                                                                                                       .16..128
/label= J_kappa_region
                                                                                                                                                                                                                                                                                                                                                                                                              Example 9; Column 41-42; 26pp; English.
                                                                               70..76
/label= CDR2
77..108
/label= frame
                                                                                                                     109..117
/label= CDR3
                                                                                                                                                                                                                              92US-0871426.
86US-0904517.
86US-0925196.
88US-0192754.
90US-0638796.
91US-0676036.
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573.00
94.31%
88.62%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 128 AA;
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                              (SANO ) SANDOZ
                                                                                                                                                                                                            05-SEP-1986;
                                                                                                                                                                                                                                                   31-OCT-1986;
11-MAY-1988;
15-JUN-1990;
27-MAR-1991;
                                                                                                                                                                   US5565354-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                             14-JUN-1994;
                                                                                                                                                                                         15-0CT-1996
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05-SEP-1986
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This is the amino acid sequence of the light chain variable (VI) region from the human monoclonal antibody (MAb) ZM1-2. The MAb was generated by immunising humans with a hepatitis B virus (HBV) vaccine, isolating peripheral blood lymphocytes (PBL) and fusing them with a mouse/human xenogeneic cell line SPAZ-4. 5 cell lines were isolated: PE1-1, ZM1-1, ZM1-2, MD3-4 and LO3-3. The cell lines were then tested for production of an anti-hepatitis B virus surface antigen antibody by ELISA. The MADS are then purified from large scale cell culture by protein A chromatography, size separation on Sephcryl 300 gell and ion exchange chromatography on Q-Sepharose. The heavy and light chains of the MADS were isolated and their amino acid sequences determined. Primers were generated and used to amplify CDNA synthesized from RNA purified from each hybridoma cell line. The sequences of the heavy and light chains (nucleic acid and amino acid) from MADS PE1-1, ZM1-1, ZM1-2 and MD3-4 are shown in AATSSSB3-45 and AAW42984-91. The MADS can be used to treat HBV infections in immunosuppressed patients or patients with chronic active hepatitis, especially liver transplant patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 ACCCAGTCTCCATCTTCCGTGTCTGCTAGGAGACAGAGTCACCATCACTTGTCGG
                               Treatment of hepatitis B - with human monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of chimpanzee Vkappa cDNA clone 46-8.
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109
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                            Example 8; Column 21-24; 25pp; English
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573.00
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88.62%
82.09%
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                                                                                                                                                                                                                                                                                                                                                                    128 AA;
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Best Local Similarity:
 AAT85844
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DB:
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ID AAYS
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GTCACCATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCAT 180
                                                                                                                                                                                                                                                                                                                                                                                                The invention provides an antibody (Ab) comprising donor CDRs (complementarity determining regions) derived from a non-human antigenspecific donor antibody, and an acceptor framework from a non-human primate. The Abs are prepared by grafting CDRs from a non-human antigenspecific donor antibody onto homologous Old World ape or monkey acceptor specific donor antibody onto homologous Old World ape or monkey acceptor frameworks. The Abs have reduced immunogenicity and are better tolerated in humans (because of the close similarity between the human and primate proteins), but retain the full antigen-binding affinity of the donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibodies containing donor complementarity determining regions and non-human primate acceptor frameworks, having reduced immunogenicity in
             Complementarity determining region; antibody; primate; immunogenicity; Old World ape; Old World monkey; antigen-binding affinity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGACATGATGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTTCTGGTTCCCAGGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetAspMetArgValProAlaGInLeuLeuGIyLeuLeuLeuLeuCysPheProGlyAla
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                               99WO-US09131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.56e-51
573.00
92.25%
86.05%
82.09%
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Query Match:
                                                                                                                                                                                                                                                                              N-PSDB; AAZ39325
                                                          Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                      WO9955369-A1
                                                                                                                                               28-APR-1999;
                                                                                                                                                                            28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                 04-NOV-1999.
                                                                                                                                                                                                                                     Taylor AH;
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CCATCAAGGTTCAGCGCCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG

CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTT

121

RESULT 12 **ABG35326**

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ABG35326;

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GTCACCATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCAT 180
                                                                                                                                                                                            81 ProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrleSerSerLeu 100
                                                                                                                                                                                                                                     CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTT 360
                                                                                                                                                                                                                                                             101 GlnProAspAspPhcAlaThrTyrTyrCysGlnGlnTyrSerAsnTyrProLeuThrPhe 120
      21 LysCysAspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerIleGlyAspArg
                                                          181 AAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                         CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anticancer human monoclonal antibody variable region sequences - and related DNA and RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; tumour antigen; cancer; monoclonal; antibody; light chain;
variable region; medicine; pharmacology; biochemistry; CDR;
complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human anti-tumour antigen antibody light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a human anti-tumour antigen monoclonal antibody (MAb) light chain variable region, useful medicine, pharmacology and blochemistry. The isotype of a MAb secreted by the human/human hybridoma HT was determined to be and kappa. Human MAb was purified, and the antigen recognised
                                                                                                                                                                                                                                                                                                   1.22
/label= sig_peptide
23.132
/label= mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                   AAW22842 standard; Protein; 132
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/label= CDR_1
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/label= CDR_2
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/label= CDR_3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT75423
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                                                                                                                                                                                                                                     301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGACATGATGCCCCGCTCAGCTCCTGGGGCTCCTGCTCTGGTTCCCAGGTTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a modified antibody comprising at least 2 heavy chain variable domains and 2 or more light chain variable domains of an antibody, and exhibite thrombopoietin (TPO) agonistic effect by causing the TPO receptor to crosslink. The antibodies are useful in preventives and/or remedies for plateler reduction-associated blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia. The antibody can act as a TPO signal transduction agonist by transducing a signal into cells by crosslinking a TPO receptor to exert TPO agonism. This is the amino acid sequence of a thrombopoietin (TPO) agonist antibody associated protein.
                                                                                                                                                                                                                       Modified antibody; thrombopoietin; TPO; agonist;
TPO receptor; platelet reduction-associated blood disease;
thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Degraded thrombopoietin agonist antibodies containing H and L chain V domains of monoclonal antibody, useful in preventives and/or remedies for blood diseases, thrombocytopenia following cancer chemotherapy or
                                                                                                                                                                                          Thrombopoietin agonist antibody associated protein #20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Orita T;
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Matches:
Conservative:
Mismatches:
Indels:
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                 GGCCAGGGGACCAAGCTGGAGATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-728-463B-206 (1-388) x ABG35326 (1-129)
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                                                                                            ABG35326 standard; Protein; 129
                                                                                                                                                                                                                                                                                                                                                                                                                     20-OCT-2000; 2000JP-0321821.
17-APR-2001; 2001WO-JP03288.
12-SEP-2001; 2001JP-0277314.
                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-2001; 2001WO-JP09259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.96e-51
                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   571.00
90.70%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsuchiya M, Ohtomo I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-383513/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABK71378
                                                                                                                                                                                                                                                                                                                         WO200233072-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                             30-JUL-2002
                                                                                                                                                                                                                                                                                          Homo sapiens.
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Alignment Scores:

Query Match: DB:

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Sequence

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The present invention relates to modified antibodies. The antibodies contain two or more H chain V domains and two or more L chain V domains of a monoclonal antibody (MAD) which is capable of transmitting a signal across the cell membrane by cross-linking a cell surface molecule, where the antibodies can serve as signal transmission agonists. The antibodies are useful for treatment and prevention of a broad range of disorders in which signal transmission is implicated, such as cancer, inflammation, hormmonal disorders, leukaemia, malignant lymphoma, aplastic anaemia, and skeletal malformations. The present sequence was used to illustrate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
ovarian cancer; breast cancer; reproductive system disorder;
infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. LysCysAspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerIleGlyAspArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCACCATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATGCGACATCCCAGATGACCCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGACATGATGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTGGTTCCCAGGTTCC
                                                           agonist
                                          Antibodies for treatment of diseases associated with cell proliferation, hormonal disorders and cytokines comprise activity to signal transmission across cell membranes
                                                                                                                                                                                                                                                                                                                                         134
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
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                                                                                                       Disclosure; Page 164; 173pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                           9.03e-51
                                                                                                                                                                                                                                                                                                                                                       571.00
90.70%
82.95%
81.81%
23
   2002-066368/09
                                                                                                                                                                                                                                                                  present invention.
                                                                                                                                                                                                                                                                                               134 AA;
                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                N-PSDB; ABA04572
                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                                                                                               Sequence
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antibody; signal transmission; cancer, inflammation; hormonal
leukaemia; lymphoma; aplastic anaemia; skeletal malformation.
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western blotting.
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CLN"-1gM.identified by
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20-OCT-2000; 2000JP-0321821.
20-OCT-2000; 2000JP-0321822.
12-MAR-2001; 2001WO-JP01912.
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                                                                                                                 Best Local Similarity:
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antibody, signal
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                                                                                                    Percent Similarity:
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KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; kW inflammatory condition; immune disorder; blood disorder; acardiovascular disorder; respiratory disorder; disorder; gastrointestinal disorder; urinary system disorder; drug screening; kW gastrointestinal disorder; urinary system disorder; drug screening; kW matipody preparation; cytostatic; immunomodulatory; neuroprotective; kW antiinflammatory; gynaecological; reproductive; chromosome 2p12. XX MO200200677-A1.

XX WO200200677-A1.

XX WALTON-2002.

XX WO-JUN-2001; 2001WO-US18569.

XX WALTON-2000; Z000US-209467P.

XX WALTON-2001; Z001WO-USI8569.

Birse CE, Rosen CA; WPI; 2002-147878/19. N-PSDB; ABQ54241. Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases -

Claim 11; SEQ ID No 2296; 2922pp; English.

Search completed: June 3, 2003, 09:02:18 Job time : 28.263 secs

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also commonsases polypeptides 90% identical and polynucloctides 95% identical to the sequences of the invention. The invention additionally relates to to the sequences of the invention. The invention additionally relates to polynucleotides, antibodies against human ovarian antigens and the use convarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, copyratic ovary syndrome, ovarian cysts, and dysmenorthoes), endocrine (e.g., infertility, disorders of pregnancy, anovulation, copyratic ovary syndrome, ovarian cysts, and dysmenorthoes), inflammatory conditions (e.g., mastitis, ophoritis and immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), crepitatory disorders (e.g., candiovascular disorders in autoimmune ophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anamina), cardiovascular disorders and urinary system disorders. Ovarian antigen polypeptides may also be used in screening for compounds which crepitate ovarian antigen sorters of compounds which turther be used as food additives or to prepare antibodies cuseful in disease diagnosis, drug targeting and phenotyping. The present cuseful in disease diagnosis, drug targeting and phenotyping. The present compounds human ovarian antigen of the invention.

Compensation, but was obtained in electronic format directly from WIPO compounds and the compounds human ovarian antigen of the invention of the printed compounds human ovarian antigen of the invention.

Sequence 260 AA;

Alignment Scores:
Pred. No.:
Score:
Score:
Score:
Percent Similarity:
Best Local Similarity:
P1.52*
Mismatches:
DB:.
23 Gaps:
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Pred. No. 1.65e-50

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Matches:
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US-08-728-463B-206 (1-388) x ABP41164 (1-260)

1 ATGGACATGATGGTCCCGGTCAGCTCCTGGGGCTCCTGCTGGTTCCCAGGTTCC 60	25 MetAspMetArgValProAlaGinLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAla 44	61 AGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGA 120	45 ArgCysAsplleClnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 64	121 GTCACCATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCAT 180	65 ValthrilethrCysArgAlaSerGlnSerIleSerAsnTyrLeuAsnTrpTyrGlnGln 84	181 AAACCAGGAAAGCCCCTAAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC 240	85 LysProGlyLysAlaProLysLeuLeulleTyrAlaAlaSer***LeuGlnSerGlyVal 104	241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCCACCATCAGCAGCTG 300	105 ProSerArgPheSerGlySerGlySerGlyThrAgpPheThr***ThrIleSerSerLeu 124	301 CAGCCIGAAGATTTTGCAACTTACTATTGTCAAGGCTAATAGTTTCCCGTACTTTT 360	125 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrAspAsn***ProLeuThrPhe 144	361 GGCCAGGGACCAAGCTGGAGTCAAA 387	145 Gly***GlyThrLygValGluleLyg 153	
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APPLICANT: TSUJİ, TARASHİ
APPLICANT: TSUJİ, TARASHİ
APPLICANT: TSUJİ, TARASHİ
APPLICANT: HOTİ, NO. US2002102558ALUAKİ
ITILE OF INVENTION: HUMAN MONOCICANLA ANTIBODY AGAINST A
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
ITILE OF INVENTION: PHARMACEUTICAL USE THEREOF
ILLE REPERBENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT APPLICATION NUMBER: US 2001-99508
PRIOR PELLING DATE: 2001-05-16
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 30
                                                                                                                                                                                                                           Sequence 92, Appli
Sequence 2, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 17, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
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Sequence 7, Appli
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Sequence 88, Appl
Sequence 10, Appl
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Sequence 6, Appli
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Sequence 2017, P
Sequence 2019, P
Sequence 2020, P
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Sequence 2003,
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10 US-09-740-002-26

9 US-10-281-349-71

10 US-09-880-748-1881

10 US-09-880-748-1881

10 US-09-86-543-10

9 US-10-288-349-88

10 US-09-056-160B-12

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     ORGANISM: Homo sapiens
     Alignment Scores:
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                                                                                                           Command line parameters:
-MODEL=frame+ n2p model - DEV=xlp
-G-Ggn2 1/USFTO_spool/US08728463/runat_03062003_085618_16959/app_query.fasta_1.3690
-G-Ggn2 1/USFTO_spool/US08728463/runat_03062003_085618_16959/app_query.fasta_1.3690
-DB=Published_Applications_AA -QFPMT=fastan -SUFFIX=xepb -MINMATCH=0.1
-LOOPELSO -LOOPEXT=0 -UNITS=bits -START=1 -RND=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR MAX=100
-THR_NIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pct -NORM=ext -HEAPSTEE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US08728463 @CGN 1 1 51 @runat 03062003 085618 16959
-NCPU=5 -NOWELOG -DEV TIMEOUT=120 -WARROUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=0.5 -DELOP=6 -DELEXT=7
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Sequence 24, Appl
Sequence 26, Appl
Sequence 69, Appl
                                                                                                                                                                          3, 2003, 09:04:15 ; Search time 16.4856 Seconds
   (without alignments)
   4764.744 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                               ATGGACATGATGGTCCCCGC......GACCAAGCTGGAGATCAAAC 388
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

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12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-740-002-24
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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       MetGluThrProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAlaArgCys 20
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Sequence 26, Application US/09855271
Sequence 26, Application US/09855271
Sequence 26, Application US/09855271
Sequence 26, Application US/0985271
Sequence 10: US20020042089A1
SEQUENCANT: Bodmer, Mark W
APPLICANT: Bodmer, Diljeet Singh
APPLICANT: Emtage, John Spencer
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
CURRENT APPLICATION NUMBER: US/09/855,271
CURRENT FILING DATE: 1999-07.02
CURRENT FILING DATE: 1999-07.02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
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COTHER INFORMATION: No. US20020042089Alel Sequence

US-09-855-271-26
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ORGANISM: Artificial Sequence
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Sequence 24, Application US/09740002

Ratent No. US20020001798A1

APPLICANT: BRAMS, PETER

APPLICANT: MORROW, PHILLIP

TITLE OF INVENTION: MEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

CURRENT APPLICATION WUMBER: US/09/740,002

CURRENT APPLICATION NUMBER: 09/335,697

PRIOR APPLICATION NUMBER: 09/488,376

PRIOR APPLICATION NUMBER: 09/488,376

PRIOR PILING DATE: 1999-06-18

PRIOR PILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTING NOS: 27

TYPE: PRI
                                                                                                                                                             61 AGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGA 120
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       Percent Similarity:
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GENERAL INFORMATION:

APPLICANT: RRAMS, PETER

APPLICANT: MORNOW, PHILLIP

ITILE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

FILE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

CURRENT APPLICATION NUMBER: US/09/740,002

CURRENT FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 08/335,697

PRIOR PELLING DATE: 1999-06-18

PRIOR FILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATCHTIN VET. 2.1

SEQ ID NO 26

LENGTH: 234

TYPE: PRI
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101 GlnProGluAspPheAlaThrTyrTyrCysGlnAsnValLeuAsnThrProLeuThrPhe 120
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Mismatches:
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                                                                                                                           Gaps:
                                                                                                    361 GGCCAGGGGACCAAGCTGGAGATCAAA
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526.50
91.47%
79.07%
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Best Local Similarity:
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Pred. No.:
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                                                                                                    81 ArgPheSerGlySerGlySerAlaThrAspTyrThrLeuThrIleSerSerLeuGlnPro 100
                                                                                                                                                                   307 GAAGATITIGCAACTIACTATIGICAACAGGCTAATAGTITCCCGTACATTITGGCCAG 366
                                                                                                                                                                                             121 GTCACCATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCAT 180
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                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-10-006-593-69
Sequence 69, Application US/10006593
Fublication No. US20030049683A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Reneblaw, Mark
ITILE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
PRIOR PELICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR FILING DATE: 2000-12-05
PRIOR PLICATION NUMBER: US 60/286,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR PLING DATE: 2001-05-09
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6: 118
SEQ ID NO 6: DE DEN FER PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PATENT OF THE PAT
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Conservative:
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                                                                                                                                                                                                                                                                      367 GGGACCAAGCTGGAGATCAAA 387
                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: artificial sequence
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86.82%
80.62%
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Pred. No.:
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67 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTTCTGCATCTGTAGGAGACAGAGTCACC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60
                                                                        247 AGGTTCAGCGCCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
        187 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCTAGCAAAGTGGGGTCCCATCA
                              61 GlyLysAlaProLysLeuLeuIleTyrHisThrSerArgLeuGlnSerGlyValProSer
                                                                                              GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCCGTACACTTTTGGCCAG
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                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09798058
Patent No. US2002009523A1
GENERAL INFORMATION:
APPLICANT: Vauchan, Tristan John
APPLICANT: Wilton, Alison Jane
APPLICANT: Walton, Alison Jane
APPLICANT: Walton, Sarah Helen
APPLICANT: Main, Sarah Helen
TITLE OF INVENTYON: Human antibodies against eotaxin and their use
FILE REFERENCE: 84632-000100
CURRENT FILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-08-29
PRIOR PLLING DATE: 2000-03-03
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103
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Matches:
Conservative:
Mismatches:
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521.50
97.22%
95.37%
74.71%
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 109
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-09-798-058-4
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                                            F. KOIKE, Macue...
FURUTA, Akiko
NAKAMURA, Kazuyasu
IIDA, Akihiro
HANAI, No. US20030096977Aluo
HANAI, No. US20030096977Aluo
FAKATSU, Kiyoshi
OF INVENTION: Antibody Against Human Interleukin-5
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FILING DATE: 90-MAY-1997
FILING DATE: 10-MAY-1997
APPLICATION NUMBER: US/08/816,561
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: LAWYENCE, III, STANTON
NAME: LAWYENCE, III, STANTON
TELEPRANION NUMBER: 25,736
REGISTRATION NUMBER: 25,736
TELEPRANICATION INFORMATION:
TELEPRANIE: 112-790-9090
TELEPRANIE: 112-790-9090
TELEPRANIE: 112-790-9090
TELEFRANIE: CONTRANIE
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Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-283-349-71
Sequence 71, Application US/10283349
Publication No. US20030096977A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 127 amino acids
TYPE: amino acid
                                                APPLICANT: KOIKE, Masamichi
                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                               NUMBER OF SEQUENCES: 106
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524.00
85.83%
81.10%
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Best Local Similarity:
Query Match:
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APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
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FILING DATE: 09-MAY-1997
APPLICATION NUMBER: UP 232384/95
FILING DATE: 11-SEP-1995
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 88:
                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING.SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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TYPE: amino acid
STRANDEDNESS: single
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TELEFAX: 212-869-9741
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: 88
SEQUENCE CHARACTERISTICS
                                                        NUMBER OF SEQUENCES: 10-
CORRESPONDENCE ADDRESS:
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85.04%
78.74%
72.92%
                                                                                                                              CITY: New York STATE: NY
                                                                                                                                                                    COUNTRY: USA
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Best Local Similarity:
Query Match:
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Pred. No.:
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-25
NUMBER OF SEQ ID NOS: 3239
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Mismatches:
Indels:
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IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, No. US20030096977Aluo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                   Sequence 1881, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 88, Application US/10283349
Publication No. US20030096977A1
GENERAL INFORMATION:
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FURUYA, Akiko
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513.00
92.79$
90.09$
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Best Local Similarity:
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RESULT 8
US-09-880-748-1881
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Pred. No.:
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LENGTH: 244
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67 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 126
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| MetMetSerSerAlaGlnPheLeuGlyLeuLeuLeuLeuCysPheGlnAspIleArgCys
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TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lawrence, III, Stanton T
REGISTRATION UNDBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                               ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
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141 GlySerGlyGlyGlyGlyGlyGlyGlyGlyGsrAspileGlnMetThrGlnSerPro 160 91 TCTTCCGTGTCTGCATCTGAGGAGACAGAGTCACTTGTCGGGCGAGTCAGGAT 150 161 SerSerLeuSerAlaSerValGlyAspArgyValhrlleThrCyGragalaSerGlnAsp 180 161 SerSerLeuSerAlaSerValGlyAspArgyValhrlleThrCyGragalaSerGlnAsp 180 161 ATTACCAGCTGGTTAGCAGGAAACCCGGAAAGCCCCTAAGCTCGTGATC 210 161 IleGlyAsnSerLeuThrTrpTyrGlnGlnLy98PcGlyLy8ThrProLy8LeuGulle 200 211 TATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGG 270 161 IleGlyAsnSerLeuThrTrpTyrGlnGlnLy98PcGlyLy8ThrProLy8LeuGulle 200 201 TATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGG 270 161 IleGlyAsnSerLeuThrTrpTyrGlnGlnLy98PcGlyLy8ThrTrgCAACTTACTAGTGG 270 201 TATGCTGCATCAGCTGGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTAGTGGG 270 201 TyrAlaThrSerSerLeuAspSerGlyValProSerArgPheSerGlySerGlySerGlySerGlySerGlySerGlyAspAfflyIleGlyAspAfflyThrTyTGGAACTTACTATTGT 330 221 ThrAspPheThrThCCGTACCATTTGCGAAGGTTACTATTGT 330 231 CAACAGGCTAATAGTTTCCGTACCATTTTGCCAACGAACACTGAACATAGTAGTAGTAGTAGTAGTAGTATTGTAAAGTAGTAAAAGTAGT	RESULT 11 US-10-268-501-5 ; Sequence 5, Application US/10268501 ; Bequence 5, Application US/10268501 ; Bublication No US20030086924A1 ; GENERAL INFORMATION:	Ø)	ty: 50.00 50.26 3x1ty: 96.26 72.21 9 9 10.1388) x US	Qy 67 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAC	
Qy 307 GAAGATTTTGCAACTGACAGGCTAATACTTTCCCGTACACTTTTGGCCAG 366 Db 101 GluAspPheAlaThrTyrTyrCysGlnGlnGlyTyrThrLeuProTyrThrValGlyGln 120 Qy 367 GGGACCAAGCTGCAGATCAAA 387 Db 121 GlyThrLysValGluIleLys 127 RESULT 10 US-09-766-543-10 58quence 10, Application Sequence 10, Application US/09766543 Fatent No. US20020041865A1 58quence Sequence 10, Application US/09766543 Fatent No. US20020041865A1 APPLICANT: RESULT No. US20020041865A1 APPLICANT: Sequence 10, Application US/09766543 Fatent NoW Cheuk APPLICANT: Rwok, Cheuk S. TITLE OF INVENTION: METHODS FILE REFERENCE: PROLOTYON CURRENT FILING TOWENTY FILING FILING PRIOR SEO 1D NOS: 14 NUMBER 60/177, 258 NUMBER 10 <td>SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 10 LENGTH: 267 TYPE: PRT ORGANISM: Artificial Sequence ORGANISM: Artificial Sequence FERTURE: OTHER INFORMATION: Description of Artificial Sequence OTHER INFORMATION: LL-2-antibody fusions OTHER INFORMATION: LL-2-antibody fusions OTHER INFORMATION: 1L-2-antibody fusions ed. No.: 6.17e-36 Length: core: 505.00 Matches: precent Similarity: 44.40% Conservative: precent Similarity: 43.24%</td> <td> Actor 130 13</td> <td>61 AG 21 AL 66</td> <td>Db 61 GlnalaProGlyGlnGlyLeuGluTrpMetGlyTrplleAsnThrTyrThrGlyGlnSer 80 Qy 66</td> <td>Qy 66 Db 101 AlaTyrMetAspLeuArgSerLeuArgSerAspAspThrAlaValTyrTyrCysAlaArg 120 Qy 66 Db, 121 ArgPheGlyPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerSerGlyGlyGly 140 Qy 67</td>	SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 10 LENGTH: 267 TYPE: PRT ORGANISM: Artificial Sequence ORGANISM: Artificial Sequence FERTURE: OTHER INFORMATION: Description of Artificial Sequence OTHER INFORMATION: LL-2-antibody fusions OTHER INFORMATION: LL-2-antibody fusions OTHER INFORMATION: 1L-2-antibody fusions ed. No.: 6.17e-36 Length: core: 505.00 Matches: precent Similarity: 44.40% Conservative: precent Similarity: 43.24%	Actor 130 13	61 AG 21 AL 66	Db 61 GlnalaProGlyGlnGlyLeuGluTrpMetGlyTrplleAsnThrTyrThrGlyGlnSer 80 Qy 66	Qy 66 Db 101 AlaTyrMetAspLeuArgSerLeuArgSerAspAspThrAlaValTyrTyrCysAlaArg 120 Qy 66 Db, 121 ArgPheGlyPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerSerGlyGlyGly 140 Qy 67

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307 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366
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                                                                                               307 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG
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                         AGGTTCAGCGCCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                           Sequence 6, Application US/09811123
; Sequence 6, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
    APPLICANT: Ralph Schwall
; APPLICANT: Ralph Schwall
; APPLICANT: Ralph Schwall
; TITLE OF INVENTION: MATHODOY-MAYTANSINOID CONJUGATES
; TITLE OF INVENTION: MATHODOY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/228,327
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR PLILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
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, OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-6
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ORGANISM: Artificial Sequence
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504.00
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90.65%
72.21%
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Best Local Similarity:
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Pred. No.:
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US-09-811-123-6
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LENGTH: 109
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97
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 0/054,856
FILING DATE: 06-Aug-1997
APTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 29,018
REGISTRATION NUMBER: 20,038.2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAY: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTER STICS:
LENGTH: Amino Acid
TYPE: Amino Acid
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                 Sequence 12, Application US/09056160B
Fatent No. US2002032315Al
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
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                                                          367 GGGACCAAGCTGGAGATCAAA 387
                                                                              101 GlyThrLysValGlulleLys 107
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
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504.00
96.26%
90.65%
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US-09-056-160B-12
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Pred. No.:
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DB:
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127 ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA
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497.00
91.89%
88.29%
71.20%
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AIGAIGGICCCCGCICAGCICCIGGGGCICCIGCIGCICTGGIICCCAGGIICCAGAIGC
                                                                                                                                                                                                Human Interleukin-5
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 7005-115-999
                                                                                                                                              ANAZAWA, Hideharu
HANAI, No. US20030096977Aluo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Hume
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                          CURPLING TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
CLASSIPICATION: CUNKNOWN>
                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
BLING DATE: 09-MAY-1997
APPLICATION NUMBER: UP 232384/95
FILING DATE: 11-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 92:
                                                                                                  FURUYA, Akiko
NAKAMURA, Kazuyasu
IIDA, Akihiro
                                  Sequence 92, Application US/10283349
Publication No. US20030096977A1
GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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77.178
71.358
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ZIP: 10036
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Best Local Similarity:
Query Match:
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                   US-10-283-349-92
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Pred. No.:
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Sequence 2, Application US/09968561A

Batent No. US200201644642A1

Batent No. US200201644642A1

Batent No. US200201644642A1

APPLICANT: Tomlinson, Ian M

APPLICANT: Winter, Gregory

TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands

CURRENT APPLICATION NUMBER: US/09/968,561A

CURRENT APPLICATION NUMBER: US 60/065,248

FRIOR APPLICATION NUMBER: US 60/065,248

PRIOR APPLICATION NUMBER: US 60/066,729

PRIOR APPLICATION NUMBER: US 60/066,729

PRIOR PILING DATE: 1997-11-21

PRIOR PELING DATE: 1997-11-21

PRIOR PELING DATE: 1998-10-20

PRIOR FILING DATE: 1998-10-20

PRIOR SPELICATION NUMBER: US 09/511,939

PRIOR SEQ ID NOS: 350

SOFTWARE: Patentin Version 3.1

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                                                                                                                                                                        GAAGATITIGCAACTIACTATIGTCAACAGGCTAATAGTITCCCGTACACTITIGGCCAG 366
                                                                                   61 GlyLysAlaProGluLeulleTyrHisThrSerArgLeuGlnSerGlyValProSer 80
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247 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                        187 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCATAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 GACAGAGTCACCATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 GGITCCAGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-728-463B-206 (1-388) x US-09-968-561A-2 (1-240)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
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189 GlyValProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 208

295 AGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTAC 354

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Search completed: June 3, 2003, 09:51:15 Job time: 18.4856 secs

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SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
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Sequence 46,
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Sequence 1
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Sequence 1
Sequence 1
Sequence 2
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Sequence
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ZIP: 9411-3834

COMPUTER READABLE FORM:
MEDIUM YYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
FILING DATE: 14-JUN-1994
CLASSIFICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION NUMBER: US 07/871,436
APPLICATION NUMBER: US 07/871,436
APPLICATION NUMBER: US 07/676,036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Townsend and Crew LLP
Center, Eighth Floor
US-08-836-561-71

US-07-934-373C-3

US-08-437-642B-3

US-08-146-206C-3

US-08-135-8

US-08-135-8

US-08-569-147-78

US-08-812-566-16

US-08-812-566-16

US-08-812-566-16

US-08-812-566-16

US-08-812-566-16

US-08-812-566-16

US-08-812-566-16

US-08-812-561-88

US-08-812-566-16

US-08-812-586-16

US-08-821-751A-2

US-08-649-100-33

US-08-462-939-37

US-08-462-939-37

US-08-462-938-164A-2

US-08-452-164A-2

US-08-157-370-3

US-08-157-370-3

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US-08-157-370-3
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Sequence 14, Application US/08259372A
Sequence 14, Application US/08259372A
FATEL NEORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HI TITLE OF INVENTION: ANTIBODIES SPECINOMER OF SEQUENCES: 16
CORRESPONDENCES: 16
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Two Embarcadero Center, E.
STREET: Two Embarcadero Center, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 27-WAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
  S
  494.5
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    Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2 1/USPTFO spool/US08728463/runat 03062003 085615 16867/app query.fasta_1.3690
-DB=168ued_Patenter AA -OFWT=fastan -SUFFIX=rai -MINMATCH=0.1 -LAOPECL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -TMATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LCOAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -NAXLEN=2000000000
-USER=US08728463_@CGN 1 1 97 @runat 03062003 085615 16867 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 185, App
Sequence 80, Appl
Sequence 6, Appli
                                                                                       3, 2003, 09:02:35 ; Search time 8.83156 Seconds (without alignments) 2585.294 Million cell updates/sec
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Sequence 2, M
Sequence 5, M
Sequence 26, N
Sequence 26, N
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Sequence 185,
                                                                                                                                                           698
1 ATGGACATGATGGTCCCCGC......GACCAAGCTGGAGATCAAAC 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                   protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-259-372A-14
US-08-468-671-14
US-08-127-918-2
US-08-470-139-26
US-09-347-061-26
US-09-042-353-48
US-08-053-131-185
US-08-053-131-185
US-08-056-147-80
US-08-659-147-80
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                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                              US-08-728-463B-206
                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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77.8
77.2
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76.2
76.2
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Percent Similarity:
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Pred. No.:
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DB:
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Patent No. 5648077
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend and Townsend and Townsend and Townsend and Townsend and Townsend STREET:
ADDRESSEE: Townsend and Townsend and Crew LIP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
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Matches:
Conservative:
Mismatches:
FILING DATE: 11-MAY-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986

PRIOR APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SED-1986
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 576-0300
TELEFAX: (415) 576-0300
TELEFAX: (415) 576-0300
TELEFAX: (415) 26-2400
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373.00
94.31%
88.62%
82.09%
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity:
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79 ACCCAGICICCAICITCCGIGICIGCAICIGIAGGAGACAGAGICACCAICACITGICGG 138
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COMPUTER: USAA

ZIP: 94111-3834

COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
CLASSIPICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 27-MAR-1991
PRICK APPLICATION NUMBER: US 07/872,754
FILING DATE: 15-JUN-1990
PRICK APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRICK APPLICATION NUMBER: US 06/925,196
FILING DATE: 11-MAY-1988
PRICK APPLICATION NUMBER: US 06/925,196
FILING DATE: 11-MAY-1988
PRICK APPLICATION NUMBER: US 06/925,196
FILING DATE: 11-MAY-1988
PRICK APPLICATION NUMBER: 30-023
APPLICATION NUMBER: 30-23
APPLICATION NUMBER: 30-23
REGISTRATION NUMBER: 30-23
REGISTRATION NUMBER: 30-23
REGISTRATION NUMBER: 30-23
REGISTRATION NUMBER: 11823-50-7
TELECOMMUNICATION INPORMATION:
REGISTRATION NUMBER: 30-23
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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Mismatches:
Indels:
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Matches:
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
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88.62%
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241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
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                         181 AAACCAGGGAAAGCCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: KURIHARA, TATSUYA
APPLICANT: KURIHARA, TATSUYA
APPLICANT: TSURUOKA, NOBUO
APPLICANT: TSURUOKA, NOBUO
APPLICANT: ARIMA, KENJI
APPLICANT: NISHIHARA, TATSURO
TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
TITLE OF INVENTION: PLASMIDS THEREFOR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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104
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13
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APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
CLASSIFICATION: 530
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 35843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-728-463B-206 (1-388) x US-08-157-101A-5 (1-236)
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: PILLSBURY, MADISON & SUTRO STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                     361 GGCCAGGGACCAAGCTGGAGATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 5, Application US/08157101A; Patent No. 5808032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.56e-53
553.00
89.92%
80.62%
79.23%
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202-822-0944
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MEDIUM TYPE: Floppy
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61 AGATGCGACATCCAGATGACCCAGTCTCCATGTTCCGTGTCTGCATCTGTAGGAGACAGA 120
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                                                                             319 ACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAGGGGACCAAGCTG 378
                                                                                                    1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 LysCysAspileGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArg 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,918
FILING DATE: 24-MAR-1994
CLASSIFTATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SMICH, Willaim M.
REGISTRATION NUMBER: 30,23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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107
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Patent No. 5506132
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LARS
TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 4
ADDRESSEE: TOwnsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 573.00
92.25%
82.95%
82.09%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                            379 GAGATCAAA 387
                                                                                                                                                                                                  125 AspPheLys 127
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
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                                                                                                                                                                                                                                                                                      Sequence 26, Application US/09347061
Patent No. 6316227
GENERAL INFORMATION:
APPLICANT: Bodmer. Mark
APPLICANT: Betting Diliest Singh
APPLICANT: Achwal, Diliest Singh
APPLICANT: Achwal, Diliest Specific Recombinant Antibodies
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
FILE REFERENCE: CARP-012
CURRENT FILING DATE: 1999-07-02
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Version 3.0
SEQ ID NO 26
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103
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Matches:
Conservative:
Mismatches:
Indels:
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NAME/KEST: misc_feature

Orlean INFORMATION: No. 6316227el Sequence
US-09-347-061-26
                                                                                                                                                                                                                        367 GGGACCAAGCTGGAGATCAAA 387
                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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543.00
89.76%
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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ATGGACATGATCCCCGCTCAGCTCCTGGGGCTCCTGCTGC
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                    361 GGCCAGGGACCAAGCTGGAGATCAAA 387
                                                                                                                                                                                                                                                                                   FILING DATE: 06 JUNE-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TRUJILLO, DOREEN YATKO
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-C
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
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543.00
89.76%
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77.79%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
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; MOLECULE TYPE: protein
US-08-470-139:26
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Best Local Similarity:
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TOPOLOGY:
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101 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrLysPheProAsnThrPheGlyGln 120
                                                                 307 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Londerg, Nils
APPLICANT: Londerg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew Lip
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/042,353
PILING DATE: 13-MAR-1996
CLASSIPICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/90,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION NUMBER: US 08/05,762
FILING DATE: 22-UL-1993
PRIOR APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/155,509
FRIENCE APPLICATION NUMBER: US 08/165,699
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APPLICATION NUMBER: US 08/544 APPLING DATE: 10-00"
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10-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 08/209,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
CMPUTER: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                          367 GGGACCAAGCTGGAGATCAAA 387
                                                                                                                                                                                 121 GlyThrLysValGluValLys 127
                                                                                                                                                                                                                                                                                           Sequence 48, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 09-MAR-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-DEC-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Embarcade
CITY: San Francisco
STATE: California
COUNTRY: USA
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61 AGAIGCGACAICCAGAIGACCCAGICICCAICTICCGIGICIGCAICTGIAGGAGACAGA 120
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Matches:
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Mismatches:
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           PRIOR AFFILIATION NUMBER: US 08/728,463
FILING DATE: 10-0CT-1996
PRIOR APPLICATION NUMBER: W0 PCT/US96/16433
FILING APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/ABORT INFORMATION:
NAME: APPLICATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARRACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                           36,429
ER: 014643-009040US
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539.00
93.16%
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amino acid
PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Best Local Similarity:
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US-08-758-417A-313
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1 AIGGACATGATGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGTTCCCAGGTTCC 60
                 AAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
                                           241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
                                                                                                                                                                          Sequence 185, Application US/08053131
Parent No. 5661016
Parent No. 5661016
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for NUMBER OF SEQUENCES: 197
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 200 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: 94105
COMPUTER: FLORM:
MEDIUM TYPE: FLORM:
MEDIUM TYPE: FLORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
CLLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, William M.
NAME: SMITH, William M.
NAME: RAITH, WILLIAM M.
REPERPRICATION UNMBER: 30,2233
REFERRENCE/COCKUT MANAGEN 30,2233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116
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Matches:
Conservative:
Mismatches:
Indels:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
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532.00
93.10%
90.52%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acid
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Best Local Similarity:
Query Match:
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US-08-053-131-185
                                                                                                                                                                                                                                                          RESULT 9
US-08-053-131-185
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Pred. No.:
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                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-728-463B-206 (1-388) x US-08-758-417A-313 (1-117)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41.303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION AUNEDR: US/08/758,417A
FILING DATE: 10-DCT-1996
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-DCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 10-DCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/165,699
FILING DATE: 22-UUL-1993
APPLICATION NUMBER: US 08/06,762
FILING DATE: 22-UUL-1993
APPLICATION NUMBER: US 08/065,762
FILING DATE: 22-UUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 08/053,131
FILING DATE: 11-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 313:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                 CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-0
INFORMATION FOR SEQ ID NO: 313
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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247 AGGITCAGCGGCAGIGGAICIGGGACAGAITICACICICACCAICAGCAGCCIGCAGCCI 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 ATCACTIGICGGGGGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KOIKE, Masamichi
APPLICANT: KOIKE, Masamichi
APPLICANT: FURUYA, Akiko
APPLICANT: NAKAMURA, Kazuyasu
APPLICANT: NAKAMURA, Hideharu
APPLICANT: ANAZAWA: Hideharu
APPLICANT: HANAI, No. 6018032uo
APPLICANT: TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
TITLE OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           127
102
9
16
0
                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-728-463B-206 (1-388) x US-08-621-751A-6 (1-127)
                NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REGISTRATION NUMBER: 32,152000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELER: 706141 MRSN FOERS SFO
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 GGGACCAAGCTGGAGATCAAA 387
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; Patent No. 6018032
                                                                                                                                                                                                                                                                                           5.946-50
526.00
87.40%
80.31%
75.36%
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                        : i27 amino acids
amino acid
                                                                                                                                                                                                                     MOLECULE TYPE: protein US-08-621-751A-6
                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: KOIKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-836-561-71
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APPLICANT: Chang, Chung N.
APPLICANT: Chandelfi, Nicholas F.
APPLICANT: Martin, Ulrich
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                     127 ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG
                                                                                                                                                                                                                                                                                               7 ATGATGGTCCCCCCTCAGCTCCTGGGGCTCCTGCTCTGGTTCCCAGGTTCCAGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/621,751A
FILING DATE: 22-MAR-1996
                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                              US-08-728-463B-206 (1-388) x US-08-569-147-80 (1-128)
                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORRISON & FOERSTER LLP
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGACCAAGCTGGAGATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08621751A Patent No. 5882644 GENERAL INFORMATION:
                                                                                                                                   2.79e-50
529.00
88.19%
81.10%
                     : 128 amino acids
amino acid
     SEQUENCE CHARACTERISTICS
                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-621-751A-6
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                                                                                      US-08-569-147-80
                     LENGTH:
TYPE: am
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DB:
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No..
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1.27e-50
532.00
93.10%
90.52%
76.22%
                LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-096-762-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                          Best Local Similarity:
Query Match:
                                                                                                                                                                         Percent Similarity:
                                                                                                                        Alignment Scores:
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                                                                                                                          121 GTCACCATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCAT 180
                                                                                                                                                                                           181 AAACCAGGGAAAGCCCCTAAGCTCCTGATGCTGCATCCAGTTTGCAAAGTGGGGTC 240
                                                                                                                                                                                                                                                                 CCATCAAGGTTCAGCGCCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 300
                                                                                                                                                                                                                                                                                     21 ArgCysAspileGlnMetThrGinSerProSerSerLeuSerAlaSerValGlyAspArg 40
                                                                                                                                              80
                                                                                                                                                                                                                 Sequence 185, Application US/08096762
Patent No. 5814318
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  301 CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTC 348
                                                                                                                                                                                                                                                                                                                                                       E: Townsend and Townsend Khourie and Crew
One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOURE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-UL-1993
CLASSIFICATION: B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US
FILING DATE: 23-UNA-1992
RIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-226-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16-DEC-1992
PRIOR APPLICATION NUMBER: US 07/00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: One Market Pl
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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AGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTGCATCTGTAGGAGAGACAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AAACCAGGGAAAGCCCCTAAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGGAGCCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 ProSerArgPheSerGlySerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
                                                                                                                                                                                                             1 ATGGACATGATGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGGTTCCCAGGTTCC 60
                                                                                                                                                                                                                                           21 ArgCygAspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40
                                                                                                                                                                                                                                                                                                                                                                                                                                301 CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,147

FILING DATE: Z5-March-1996

CLASSIFICATION: 536

ATTORNEY AGENT INFORMATION:

NAME: Trujillo, Doreen Yakko

REGISTRATION NUMBER: 35,719

REGISTRATION NUMBER: 35,719

TELECHMUNICATION INFORMATION:

TELECHMUNICATION INFORMATION:

TELEFHONE: (215) 568-3100

INFORMATION FOR SEQ ID NO: 80:
                                                                                                                                                        US-08-728-463B-206 (1-388) x US-08-096-762-185 (1-116)
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 61803/77ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 80, Application US/08569147
Patent No. 6180377
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMANISED ANTIBODIES
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
```

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
CORRESPONDENCE: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1991
ATTORNEY/AGENT INFORMATION:
RECISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                  Genentech, Inc
                                                                                                                                                       STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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517.00
97.20%
92.52%
74.07%
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Amino Acid
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GENERAL INFORMATION:
APPLICANT: Paul J
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Best Local Similarity:
                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 GluAspPheAlaThrTyrTyrTyrCysGlnGlnGlyTyrThrLeuProTyrThrPheGlyGln 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 GACATCCAGATGACCCAGTCTCCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 ATCACTTGTCGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||||||
| MetMetSerSeralaGlnPheLeuGlyLeuLeuLeuCysPheGlnAspIleArgCys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 ATGATGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCCCAGGTTCCCAGATGC 66
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Mismatches:
Indels:
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                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FASELSEQ Version 2.0
SOFTWARE: FASELSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 09-MAY-1997
CLASSIFICATION 424
PRIOR APPLICATION 424
PRIOR APPLICATION WHER: 424
PRIOR APPLICATION NUMBER: 10P23284/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: LAWFENCE, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: STORNOENESS: single
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Matches:
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; Sequence 3, Application US/07934373C
; Patent No. 5821337
                                     ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          524.00
85.83%
81.10%
75.07%
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Best Local Similarity:
Query Match:
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Pred. No.:
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247 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 186
                                                                                                                                                                                                                                                                                                                                     21 IleThrCysArgAlaSerGlnAspValSerSerTyrLeuAlaTrpTyrGlnGlnLysPro 40
                                                                                                                                                                                                                                                                                                                                                                                                                               41 GlyLysAlaProLysLeuLleTyrAlaAlaSerSerLeuGluSerGlyValProSer 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
                                                                                                                                                                                                                                         1 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr
                                                                                                                                                                                                                                                                                                                                                                                                    187 GGGAAAGCCCCTAAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGGTCCCATCA
                                                                                                                                                                                                                 67 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC
109
33
0
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                  US-08-728-463B-206 (1-388) x US-07-934-373C-3 (1-109)
                                                                                                                    Gaps:
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101 GlyThrLysValGluIleLys 107

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 ATCACTTGTCGGGGGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                  APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
CORRESPONDENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA.
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA.
APPLICATION NUMBER: 06/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA.
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
                                                                                                                                                                                                                                                                                                                                                        URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-009-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                             SYSTEM: PC-DOS/MS-DOS
WinPatin (Genentech)
                                  3, Application US/08437642B
5, 6054297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                         Genentech, Inc
                                                                                                                                                                                  South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: P
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92.52%
74.07%
                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                      STATE: C. COUNTRY:
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DB:
RESULT 15
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GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246

187

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21 IleThrCysArgAlaSerGlnAspValSerSerTyrLeuAlaTrpTyrGlnGlnLysPro 40

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Db 41 GlyLysAlaProLysLeuLeulleTyrAlaAlaSerSerLeuGluSerGlyValProSer 60

Qy 247 AGGTTCAGCGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTGCAGCT

Db 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80

Qy 307 GAAGATTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366

Db 81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerLeuProTyrThrPheGlyGln 100

Qy 367 GGGACCAAGTTGAATAGTCAAA 387

Db 101 GlyThrLysValGluIleLys 107

Search completed: June 3, 2003, 09:47:25

Job time: 10:8316 secs
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RESULT 1
PH1558
Igh heavy chain V region (clone DOB) - human (fragment)
Cypecies: Homo sapiens (man)
Cypecies: Homo sapiens (man)
Cypecies: Homo sapiens (man)
Cybecies: Homo sapiens (man)
Cybecies: Homo sapiens (man)
Cybecies: Nag-1994 #sequence_revision 05-Aug-1994 #text_change 16-Aug-1996
CyAccession: PH1558
RyRassenti, L.Z.; Kipps, T.J.
J. Exp. Med. 177, 1039-1046, 1993
AyTitle: Lack of extensive mutations in the VH5 genes used in common B cell chroparates number: PH1557; MUID:93210459; PMID:7681468
AyReference number: PH1557; MUID:93210459; PMID:7681468
AyMolecule type: DNA
AyResidues: 1-139 cARA>
CySuperfamily: immunoglobulin V region; immunoglobulin homology
CyKeywords: heterotetramer; immunoglobulin
F;32-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SerThrAlaIleLeuAlaLeuLeuLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln~20
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 139
127
7
5
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                            PH1415
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-Q=/cgn2_1/USPTO_spool/US08728463/runat_03062003_085615_16827/app_query.fasta_1.3690
-DB=PIR 73 -QPNT=fastan -SUFPTX=pr -MINMATCH=0.1 -LOOPCI_=0 -LOOPEXT=0
-UNITYS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITYS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITYS=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
-USRE=US08728463 @ccN 1 1.177 @runat 03062003 085615 16827 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=10 -LONGLOG
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127 GGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCGCCAGATGCCCGGGAAA 186

41 GlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMetProGlyLys

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Cipate: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
Cipate: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
Cipacession: PH1559
R.Rassenti, L.Z.; Kipps, T.J.
J. Exp. Med. 177, 1039-1046, 1993
A;Title: Lack of extensive mutations in the VH5 genes used in common B cell
A;Reference number: PH1557; MUID:93210459; PMID:7681468
A;Molecule type: DA.R.
A; Reference number: PH1557; MUID:93210459; PMID:7681468
A;Molecule type: DA.R.
408
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-115/Domain: immunoglobulin homology <INM>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Os-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
C;Accession: PH1562
R;Rassenti, L.Z.; Kipps, T.J.
J. Exp. Med. 177, 1039-1046, 1993
A;Title: Lack of extensive mutations in the VH5 genes used in common B cell chrc A;Reference number: PH1567; MUID:93210459; PMID:7681468
A;Reference number: PH1567; MUID:93210459; PMID:7681468
C;Supercassion: PH1562
A;Residues: 1-137 < RAS>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetzamer; immunoglobulin
F;32-115/Domain: immunoglobulin homology < IMM>
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A;Residues: 15144 <AND>
A;Cross-references: GB:M67504; NID:g185413; PIDN:AAA52946.1; PID:g185414
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroretramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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Ig heavy chain precursor V-V region (257-D) (anti-HIV-1) - human
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 19-Feb-1994 #sequence revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: S16685; S16689; S16690
R; Berman, J. B.; Humphrites, C. G.; Barth, J.; Alt, F.W.; Tucker, P.W.
J. Exp. Med. 173, 1529-1535, 1991
A; Title: Structure and expression of human germline V(H) transcripts.
A; Reference number: S16685; MUID:91237299; PMID:1903431
A; Reference number: S16685; MUID:91237299; PMID:1903431
A; Reference number: S16685
A; Molecule type: mRNA
A; Residues: 1-128 < RER.
A; Accession: S16688
A; Accession: S16688
A; Residues: 1-128 < RER.
A; Residues: 1-128 < RES.
A; Cross-references: EMBL:X58400; NID:933620; PIDN:CAA41298.1; PID:933621
A; Received: translation not shown
A; Reperimental source: clone EBV-21
A; Accession: S16689
A; Status: translation not shown
A; Received: RNBA
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(Cross-references: EMBL:X58401; NID:g33622; PIDN:CAA41299.1; PID:g33623; Experimental source: clone L2-9
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                      Length:
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Mismatches:
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A;Molecule type: mRNA
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A; Status: translatio
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: PH1565
R;Rassenti, L.Z.; Kipps, T.J.
J. Exp. Med. 177, 1039-1046, 1993
A,Title: Lack of extensive mutations in the VH5 genes used in common B cell
A,Reference number: PH1565
A,Reference number: PH1565
A,MOID: 93210459; PMID: 7681468
A,Residues: 1-138 exRAS-
A,Residues: 1-138 exRAS-
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;32-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                      41 CysLysGlySerGlyTyrSerPheThrSerTyrTrplleGlyTrpValArgGlnMetPro
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A;Residues: 1-128 <BE4>
A;Cross-references: BMBL:X58402; NID:g33624; PIDN:CAA41300.1; PID:g33625
A;Cross-references: clone CB-4
A;Experimental source: clone CB-6
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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Db. 61 GlyLysGlyLeuGluTrpMetGlyIle	C E M 0	A.Accession: PH1564 A.Molecule type: DNA A.Residues: 1-138 <ras> C.Superfamily: immunoglobulin V region; immunoglobulin homology C.Keywords: heterotetramer; immunoglobulin F;32-115/Domain: immunoglobulin homology <imm></imm></ras>	- 	9y 7 TCAAC 1 SerTh 1 S		81 307 101 367	Db 121 TyrSerGlyCysSerGlnSertrPGlJGlnGlyThrLeuValThrValSerSer 138 RESULT 9 PH1557 Ig heavy chain V region (clone 5-2R1) - human (fragment) C; Species: Homo sapiens (man) C; Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #sequence_revision 05-Aug-1996
21 127 41 187 61	Qy 247 TTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGG 306	RESULT 7 A28846 IS heavy chain precursor V region (VH251) - human C;Species: Homo sapiens (man) C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999 C;Accession: A28846; A39982	R;Humphries, C.G.; Shen, A.; Kuziel, W.A.; Capra, J.D.; Blattner, F.R.; Tucker, P.W. Natures 331, 446-449; 1988 A;Title: A new human immunoglobulin V-H family preferentially rearranged in immature B A;Reference number: A28846; MuID:88122615; PMID:3123998 A;Reseasion: A28846 A;Molecule type: DNA A;Residues: 1-117 <hum> A;Residues: 1-117 <hum> R;Shen, A; Humphries, C - Tucker D - D; Shen, A; Humphries, C - Tucker D - D; Shen, A; Humphries, C - Tucker D - D; Shen, A; Humphries, C - Tucker D - D; Shen, A; Humphries, C - Tucker D - Shen, A;</hum></hum>	Proc. Natl. Acad. Sci. U.S. Auchel, F. Alatener, F. Affilter Human heavy-chain variable region gene family nonrandomly rearranged in famili A.Reference number: A39982, MUID:88068629, PMID:3120193 A.Reference number: A39982, MUID:88068629, PMID:3120193 A.Accession: A39982 A.Status: preliminary A.Residues: prili ASHE> A.Residues: 1-117 ASHE> A.Residues: 1-117 ASHE> C.Suberfamily: immunoclobuling N. NID:9185574; PIDN:AAA53013.1; PID:9567178	C; Keywords: heterotetramer; immunoglobulin homology F;34-117/Domain: immunoglobulin homology < IMM> Alignment Scores: Fred. No.: Score: Fred. No.: S55.00 Matches: Fred. No.: S55.00 Matches: Best Local Similarity: 96.58 Mismatches: Alignment Scores: 113 Percent Gimilarity: 96.58 Mismatches: 20ery Match: 70.33* radiantches:	100 100	

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Ig heavy chain V region (monoclonal striational autoantibody StrAB SA-1A VH) - human (fr. C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
C;Accession: A49047 A40047
R;Viccor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
R;Viccor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224; PMID:1516616
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SerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln
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Ricession: PH1561
Airle: Lack of extensive mutations in the VH5 genes used in common B cell Airle: Lack of extensive mutations in the VH5 genes used in common B cell Aireference number: PH1561
Aireference number: PH1561
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Aireference number: H1561
Aireference number: Immunoglobulin V region; immunoglobulin homology
Cisuperfamily: immunoglobulin homology <IMM>
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              fitle: Lack of extensive mutations in the VH5 genes used in common B Reference number: PH1557; MUID:93210459; PMID:7681468 Accession: PH1557
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                                                         A,Molecule type: DNA
A,Residues: 1-115 <RAS>
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heteroterramer; immunoglobulin
F;32-115/Domain: immunoglobulin homology <IMM>
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Med. 177, 1039-1046, 1993
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RESULT 13 RESULT 13 PH1563 Ig heavy chain V region (clone PET) - human (fragment) C;Species: Homo sapiens (man) C;Accession: Homo sapiens (man) C;Accession: PH1563 R;Rassenti, L.Z.; Kipps, T.J. J; Rassenti, L.Z.; Kipps, T.J. J; Exp. Med. 177, 1039-1046, 1993 A;Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic A;Reference number: PH1567; MUID:93210459; PMID:7681468 A;Residues: PH1563 A;Molecule type: DNA A;Residues: 1-144 cRAS> C;Superfemily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotecramer; immunoglobulin F;32-115/Domain: immunoglobulin homology <imm></imm>	Alignment Scores: Parison to be considered to be cons	CTGGTGCAGTCTGGAGCTGAAAAAGCCCGGGGAGTCTTGAAGATCTCTTAAG LeuvalGlnSerdlyAlaGluvalLy8broGlyGluSerLeuarglleSerCygLy8 LeuvalGlnSerClyAlaGluvalLy8broGlyGluSerLeuarglleSerCygLy8 GGTTCTGGATACAGCTTTACCGCTACTGGATCGCTCGGTGCGCCCACATGCCCGGAAA 	61 GlyLeuGluTrpMetGlyArgileAspProSerAspSerTyrThrAsnTyrSerProSer 247 TTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCGCCTACCTGCAGTGG	Db 121 AlaAlaAlaTrpGlyTyrTyrTyrTyrTyrMetAspValTrpGlyLysGlyThrThrVal 140 Gy 397 ACGTCTCCTCA 408 Db 141 ThrValSerSer 144 RESULT 14 PH1414 Igheavy chain V region (clone P1-54) - human (fragment) C;Species: Homo sapiens (man) C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999 C;Accession: PH1414 R;van der Stoep, N; van der Linden, J; Logtenberg, T. J; Exp. Med. 177, 99-107, 1993 A;Title: Molecular evolution of the human immunoglobulin E response: High incidence dermacitis. A;Reference number: PH1409; MUID:93115676; PMID:8418213
Db 61 AspThrArgTyrSerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIle 80	thier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. Data Library, June 1992 Sms that generate human immunoglobulin diversity operate 1585 SL. Z14183; NID:g31033; PIDN:CAA78552.1; PID:g31034 Albelin V region; immunoglobulin homology Palobulin homology <imm></imm>	Alignment Scores: Pred. No.: Score: Score: Score: Secrent Similarity: Bs.82* Matches: Percent Similarity: Bs.82* Matches: Bs.82* Matches: Bs.82* Matches: 117 Conservative: 4 Bs.82* Mismatches: 15 Query Match: 69.09* Mismatches: 5 Indels: 5 US-08-728-463B-207 (1-462) x S31685 (1-141) Oy 1 ATGGGGTCAACCGCCATCCTCCTGGCTGTTCTCCAAGGAGTCTGTGCCGAG 60		Oy 181 GGGAAAGGCTGGATGGGATCATCTATCCTGGTGACTCTGATACCACATACAGC 240

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R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of dernatitie.
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of A;Title: Molecule rype: mRNA
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Molecule type: mRNA
A;Residues: 1-113 cvANA
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A;Residues: 1-113 cvANA
A;Cross-references: GB:S51905; NID:9262690; PIDN:AAC80261.1; PID:g262691
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hererotetramer; immunoglobulin
C;Keywords: hererotetramer; immunoglobulin homology < IMM>
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A; Residues: 1-127 < VAN>
A; Residues: 1-127 < VAN>
A; Residues: 1-127 < VAN>
A; Note: the authors translated the codon TTG for residue 119 as Met
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < IMM>
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US-08-728-463B-207 (1-462) x PH1428 (1-113)
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-!- MISCELLANBOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL (NPB ANTIBODIES).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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SEQUENCE FROM N.A.
MEDLINE-81224548; PubMed=6788376;
MEDLINE-81224548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
  CHAIN V REGION B1-8/186-2.
IG HEAVY CHAIN V REGION B1-8/1
PRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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Immunoglobulin V region; Signal.
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MEDLINE=81234548; PubMed=6788376;
MEDLINE=81234548; PubMed=6788376;
MEDLINE=81234548; PubMed=6788376;
MEDLINE=B11 A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";
-!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL (NPB ANTIBODIES).
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HSSP; P01.810; ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
Immunoglobulin V region; Signal.
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ZAKUL R., Cohen J., Givol D.;
Nucleic Acids Res. 8:4839-4840 (1980).
-!- MISCELLANDEGUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A MYELOMA THAT SECRETES IGG2B.
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HSSP, P01810, 2FBJ.
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INTERPRO; IPR003596; Ig MHC.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDLINE-81053741; PubMed-6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
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                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PIR, AAC026; HYWGG7.
HSSP, P01810; 2PBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Emming010047; ig_1 1.
SWART; SW00406; Igy. 1.
Imming010bulin V region; Antiarsonate antibody; Hybridoma; Signal.
                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                STRAIN=A/J;
MEDINE=82152818; PubMed=6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
Capra J.D.;
                                                                                                                                                                                                                                                                                                                              "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:309-311(1982).
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Mismatches:
Indels:
Gaps:
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region 93G7 precursor.
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Matches:
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|GinLeuSerSerLeuThrProGluGluPheAlaValTyrTyrCy9AlaArgSerAsp--- 119
                  CAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGAGACCAACTG 360
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| MetGlyTrpSerCysIleIleLeuPheLeuValAlaThrAlaThrGlyValHisSerHis 20
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                                                                                                                                "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
                                                                                                       GGCCTCTTTGAC-----TACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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PRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEMORK-2.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse)
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 GluLyBPheLyBAsnLyBAlaThrLeuThrValAspLysSerSerSerThrAlaTyrMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 ValGinLeuGinGinProGlyAlaGluLeuValLysProGlyAlaSerValGinLeuSer 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGGGTCAACCGCCATCCTCGCCTCCTGGCTGTTCTCCAAGGAGTCTGTGCCGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||| ::: |||::::
1 MetGlyTrpSerTyrIleIleLeuPheLeuValAlaThrAlaThrAspValH1sSerGln 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-84248078: PubMed-6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                                                                                              23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
23-OCT-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region TEPC 1017 precursor.
Mus musculus (Mouse)

Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                              "Illegitimate recombination generates a class switch from C mu to delta in an igD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
PIR; A02033; HVMST7.
INSSP; POISB10; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
SMART; SM00406; Igy; 1.
SMART; SM00406; Igy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION TEPC 1017.
RAMÜNOKK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMÜNORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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25
38
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                  138 AA
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374.00
69.78%
51.80%
                                                                                                            STANDARD;
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138 AA;
|||
Ser 121
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                            MOUSE
                      121
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DISULFID
NON TER
SEQUENCE
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                                                                                                            HV48 MO
P03980;
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InterPro, IPR003006, 1g_MHC.
InterPro, IPR003596; 1g_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J00536; AAA38605.1; -.
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366.00
76.07%
55.56%
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54
68
85
117
1115
                                                                                                                                                                                                                                               Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A02031; HVMS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6;
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DB:
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                            241 CCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACGGCCTACCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 GIGAAAAAGCCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTACC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 GGCTACTGGATCGGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGATC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LeuleuAlaValAlaProGlyAlaHisSerGlnValGlnLeuValGlnSerGlyAlaGlu 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 SerTyrTyrMetHisTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyIle 69
.
.61 GlyGlnGlyLeuGluTrplleGlyArglleHisProSerAspSerAspThrAsnTyrAsn 80
                                           GlnLysPheLysGlyLysAlaThrLeuThrValAspLysSerSerThrAlaTyrMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 CTCCTGGCTGTTCTCCAAGGAGTCTGTGCCGAGGTGCAGCTGGTGCAGTCTGGAGCAGAG
                                                                                                                                                                                                                                                                                          MEDLINE-83144028; PubMed=6298778;
Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                         CAGTGGAGCAGCCTGGAACGCCTCGGACACCGCCATGTATACTGTGCG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V-I REGION HG3.
                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12946 MW; 2D3F92FC60CD1FE7 CRC64;
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67
18
23
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Matches:
Conservative:
Mismatches:
Indels:
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Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Homo sapiens (Human).
                                                                                                                                                117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-728-463B-207 (1-462) x HV1B_HUMAN (1-117)
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J00240; AAA52988.1; -. PIR; A02024; HVHUHG.
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367.00
78.70$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.04%
43.38%
                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AA;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                            Mammalia; Euther:
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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SEQUENCE
                                                    81
                                                                          301
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                                                                                       327
                                                                                                                     "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                       268 TCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG HEAVY CHAIN V REGION 3.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPLEMENTARITY - DETERMINING - 2.
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                        328 ACCGCCATGTATTACTGTGCGAGA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region 3 precursor
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SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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178 CCCGGGAAAGGCCTGGAGGGATGGGGATCATCTATCCTGGTGACTCTGATACCACATAC 237
                                                                                                                                                                                                 238 AGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACGGCGTAC 297
                                                                                                                                                                                                                                                                                                  298 CTGCAGTGGAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGAGACAAA 357
                                                                                                                                                                                                                                                                                                                                   Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;

Lin Bach M.K. (468.);

Lin Bach M.K. (468.);

Linmediate hypersensitivity; modern concepts and developments, pp.1-36, arcel Dekker, New York (1978).

Linmediate hypersensitivity; modern concepts and developments, pp.1-36, arcel Dekker, New York (1978).

Linmediate hypersensitivity; modern concepts and developments, pp.1-36, arcel Dekker, New York (1978).

PROTEIN.

PROTEIN.

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PROMOSO (197.)

PROMOSO (197.)

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PROMOSO (197.)

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PROMOSO (197.)

PROMOSO (197.)

PROMOSO (197.)

PROMOSO (197.)

PROMOSO (197.)
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                                                                                                                           SEQUENCE FROM N.A..
MEDLINE=83065234; PubMed=6815656;
MEDLINE=81065234; PubMed=6815656;
Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
Bell L.O., Gould H.J.;
"Cloning and sequence determination of the gene for the human
immunoglobulin epsilon chain expressed in a myeloma cell line.";
proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                                                                   358 CTGGGCCTCTTTGACTACTGGGGCCAGGGAACCCTGGTCACGGTCTCCTCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                            101 TYXTrpTyrPheAspValTrpGlyAlaGlyThrThrValThrValSerSer 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V-I REGION ND. PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
1G heavy chain V-I region ND precursor (Fragments)
Homo sapiens (Human).
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VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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Matches:
Conservative:
Mismatches:
Indels:
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1 MetGlyTrpSerCysIleIleLeuPheLeuValAlaThrAlaThrGlyValHisSerGln 20
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MEDLINE=80078170; PubMed=6765983;
Schilling J., Clevinger B., Davie J.M., Hood L.;
Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
INTERESTANGENCS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
HIGHOROUS: THE DAND J SECHENTS.
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HICH OCCUR IN THE DAND J SECHENTS.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
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                                                                                                                                            1 GluValGlnLeuGlnGlnGlnSerGlyProGluLeuValLysProGlyAlaSerValLysMet
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MEDIINE=88296408; PubMed=2841108;
MEDIINE=88296408; FubMed=2841108;
MEDIINE=88296408; FubMed=2841108;
Ohno H., Fukuhara S., Honjo T.;
"Dispersed localization of D segments in the human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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(Rel. 38, Last annotation update)
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                                                                                 US-08-728-463B-207 (1-462) x HV12_MOUSE (1-117)
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01-NOV-1991 (Rel. 20, Last sequence upda 15-UUL-1999 (Rel. 38, Last annotation upda heavy chain V-I region V35 precursor.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Ffan; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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    57.26%
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117 AA;
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                                                                                                                      61 GTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATCTCC 120
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                                                                                                                                          21 ThrGlnLeuValGlnSerGlyAlaGluValArgLysProGlyAlaSerValArgValSer 40
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Biochemistry 21:5415-5424(1982)
-!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annocation update)
15-JUN-2004 (Nel. 01 wregion MOPC 104E.
Mus musculus (Mouse)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinee, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
MEDLINE=813075344; PubMed=6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
Hood L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .) (COMPLEX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Complete amino acid sequence of a mouse mu chain: homology
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-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
PIR, A02039; MHMS4R.
HSSP, P017099; INCP.
InterPro; P017099; IG MHC.
InterPro; IPR003006; Ig MHC.
Pfam; PP00047; ig; 1.
SWART; SMO0407; ig; 1.
Immunoglobulin V region; Glycoprotein.
DISULFID
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US-08-728-463B-207 (1-462) x HVIC_HUMAN (1-147)
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Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
Blattner F.R.;
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Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
15-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 138, Last annotation update)
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15078 MW; 6827CFBC6DB3F35E CRC64;
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HSSP: P01772, 2FB4.
INTERPRO; IPR003006; IG_MHC.
INTERPRO; IPR003596; IG_V.
SMART; SM00406; IG_V.
IMMUNOGlobulin V region; Signal.
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-! MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS SEGNENT, JHZ.

SEGNENT, JHZ.
PIR: A02028; HVMSG7.
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Mus musculus (Nouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
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SEQÜENCE 120 AA; 13307 MW; FF04E4A167RG64AB CPC64.
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15-JUL-1999 (Rel. 38, Last annotation update)
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InterPro, IPR003006, 19_MHC.
InterPro, IPR003596, 19_v.
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| MetGlyTrpSerCysIlellePhePheLeuValAlaThralaThrGlyValHisSerGln 20
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PIR, A02030; HWM23.
HSSP, P01810; 2FBU.
InterPro; IPR003106; Ig_WC.
InterPro; IPR003106; Ig_V.
Pfam; PF00047; ig; 1.
Immunoglobulin V region; Signal.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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Mismatches:
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Lest annotation update)
Mus musculus (Mouse)
                                                                    US-08-728-463B-207 (1-462) x HV15_MOUSE (1-136)
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61 GlyGlnGlyLeuGluTrpIleGlyAsnIleAsnProGlyAsnGlyGlyThrAsnTyrAsn 80
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Search completed: June 3, 2003, 09:04:05 Job time: 10.7633 secs

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091192 homo s

092164 mus m

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Q99125 mus r
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Q991a6 mus
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Mus musculus (Mouse).
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                            protein search, using frame_plus_n2p model
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A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Bromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Machima J., Mazzarelli J., Mombaerts P.,
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A Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Hynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hructional annotation of a full-length mouse cDNA collection.",
EMBL, AKO7918; BAB25349.1; --
R HSSP, P01842; 7FB.
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ThrSerGluAspSerAlaValTyrPheCysAlaArgSerGlyTyrAspTyrAspTrpPhe
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InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003500; Ig_like.
InterPro; IPR003500; Ig_like.
InterPro; IPR003506; Ig_WHC.
InterPro; IPR003596; Ig_V.
FAMAT; SM00407; ig; 4.
SWART; SM00407; IG; 2.
SWART; SM00400; IG; 3.
SWART; SM00400; IG; 1.
SWART; SW00410; IG like; 1.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
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Pred. No.:
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86 LysAlaLysLeuThrAlaAspLysSerSerValThrAlaPheLeuGlnLeuThrSerLeu 105
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6 IleLeuLeuPheLeuLeuSerValThrGluGlyValHisSerGlnValGlnLeuLeuGln 25
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01-JUN 2002 (TrEMBLrel. 21, Created)
01-JUN 2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 51.7 kDa protein.
Hypothetical 51.7 kDa protein.
Bus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musina
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Sciurognathi; Muridae; Murinae; Mus
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885
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
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Matches:
Conservative:
Mismatches:
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
[1]
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446.00
75.34%
58.22%
52.72%
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Best Local Similarity:
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PRT;
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434.00
70.27%
55.41%
51.30%
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                                        Chernajovsky Y.;
Submitted (OCT-2001)
                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                  SEQUENCE FROM N.A. STRAIN=BALB/C;
                    SEQUENCE FROM N.A.
NCBI_TaxID=10090;
                               STRAIN=BALB/C;
Chernalovsky Y
                                                                                                                                                                                                                                                                    Percent Similarity:
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Q8TC77;
01-JUN-2002 (
01-JUN-2002 (
01-JUN-2002 (
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                                                                                                                                                                                                                                                                                                                                                                                                       196 TGGATGGGGATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                               256 CAGGICACCAICTCAGCCGACAAGICCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTG 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45
                                                                                                                                                                                                                                                                                                                                                                              26 SerGlyAlaGluLeuAlaArgProGlyAlaSerValArgLeuSerCysLysAlaSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                            MGD, MGI:96446 igh-4.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_like.
InterPro; IPR00407; Ig. 4.
InterPro; IPR00407; Ig. 4.
SMART; SM00400; IG. 2.
R SMART; SM00400; IG. 2.
R SMART; SM00410; IG. 12.
R SMART; SM00410; IG. 11ke; I.
R SMART; SM00410; IG like; I.
R SMART; SM00410; IG like; I.
R SMART; SM00410; IG mMC; UNKNOWN I.
R PROSITE; PS00290; IG mMC; UNKNOWN I.
         Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; --
HSSP; P01842; 7FAB.
                                                                                                                                                                                               463
83
26
37
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Last annotation update)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8VDC9;
01-MAR-2002 (TrEMBLrel. 20, Cr
01-MAR-2002 (TrEMBLrel. 20, La
01-JUN-2002 (TrEMBLrel. 20, La
Anti-MOG Z12 variable gamma 2a
IGG2A.
                                                                                                                                                                                             2.83e-33
442.50
73.15%
55.70%
52.30%
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                      Alignment Scores:
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GIGCAGICIGGAGCAGAGGIGAAAAAGCCCGGGGAGICICIGAAGAICICCTGIAAGGGI 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGA-----GACCAACTGGGC 363
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|LeuGluTrpIleGlyGluIleLeuProGlySerGlyArgThrAsnTyrAsnGluLysPhe 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 ACCGCCATCCTCGCCCTCCTGGCTGTTCTCCAAGGAGTCTGTGCCGAGGTGCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 GlnGlnSerGlyAlaGluLeuMetLySProGlyAlaSerValLyS1leSerCysLysAla
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                                                                                                         "Targeting T cells to the CNS.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ416332; CAC94867.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.Wt.
InterPro; IPR003596; Ig.v.
InterPro; IPR004330; Prenyl_site.
FFMAN; SW00409; IG; 1.
SWART; SW00406; IGv; 1.
to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                   168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;
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82
22
42
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                           PROSITE, PSO0294; PREMYLATION, UNKNOWN_1.
NON TER 168 168
SEQÜENCE 168 AA; 18293 MW. 182910500000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-728-463B-207 (1-462) x Q8VDC9 (1-168)
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23

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GGAGCAGAGGTGAAAAAGCCCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATAC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 ATGGGGATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCAG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 GICACCATCICAGCCGACAAGICCAICAGCACCGCCIACCIGCAGIGGAGCAGCTGAAG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 GCCTCGGACACCGCCATGTATTACTGTGCGAGAGACCAACTGGGCCTCTTTGACTACTGG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 AGCITITACCGGCTACTGGATCGGCTGGGTGCGCCAGATGCCCCGGGAAAGGCCTGGAGTGG
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                    factor VIII inactivation: study with e
ived from a hemophilia A patient with
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                         563D164AB22802D5 CRC64;
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                  "Mechanism and kinetics of facto
IgG4 monclonal antibody derived
inhibitor.";
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150
16031 MW;
                                                                                      EMBL, AJ224083, CAA11829.1;
HSSP, P01772, 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003566; Ig_V.
                                                                                                                                                                                                                                                                                                     4.36e-32
429.00
72.34%
58.87%
50.71%
                                                                                                                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                       Blood 92:496-506(1998)
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TISSUE=SALIVARY GLAND;
Strausberg R.;
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150 1:
150 AA;
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Best Local Similarity:
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SIGNAL
NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCTACTGGATCGGCTGCGCCCAGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 TCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGGCCTGAAGGCCTCGAC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCOCCATGIATTACTGTGCGAGAGACCAACTGGGCCTC------TTTGAC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 LeuTrpGlyAkgGlyThKLeuValThrValSerSerAlaSerThrLysGlyProSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACTGGGGCCAGGGAACCCTGGTCACCGTCTCAGCCTCCAAGGGCCCATCGGTC
                                 Eukaryoča, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                         Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBJ. BC034289; AAH24289.1;
Hypothetical protein.
SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O9Y298 PRELIMINARY, PRT, 150 AA.
09Y298, 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
19G VH protein precursor (Fragment).
                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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MEDLINE=98322155; PubMed=9657749;
Jacquemin M.G., Vander Elst L.P.L.;
Hypothetical 51.8 kDa protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                       2e-32
433.50
73.65%
58.11%
51.24%
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                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                          LISSUE=SPLEEN;
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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 TCTGGATACAGCTTTACCGGCTACTGGATCGGCTGCGCCCAGATGCCCCGGGAAAGGC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 CAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 CTCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACGAGGGC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 ThrGlyTyrThrPheSerSerTyrTrpIleGluTrpValLysGlnArgProGlyHisGly 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 LeuGluTrp11eGlyGluIleLeuProGlySerGlySerThrAsnTyrAsnGluLysPhe 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
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0-1 DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 52.1 kDa protein.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               424 CCATCGGTCTTCCCCCTG------GCACCCTCCTCCAAGAAG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

RMBL; BC018315; AAH18315.1; -.

InterPro; IPR003599; Ig.

InterPro; IPR003597; Ig_c1.

InterPro; IPR003596; Ig_w.

R InterPro; IPR003596; Ig_w.

R Fam; PR00047; Ig; 2.

R SWART; SM00409; IG; 2.

R SWART; SM00409; IG; 2.

R SWART; SM00409; IG; 1.

R PROSITE; PS00299; IG_MHC; UNKNOWN_3.

HYPOCHETICAL PROCEEIN.

SEQUENCE 613 AA; 67855 WW; 41A9384DD4C22862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=COLON;
Strausberg R.; Strausberg (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                           613
86
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||:::|||:::|||:::
81 GluLysPheLysGlyLysThrThrLeuThrAlaAspLysSerSerThrAlaTyrMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 CAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGAGACCAACTG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 PheLeuSerSerLeuThrSerGluAspSerAlaValTyrPheCysThrArgGlyGlyGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 GGCCTCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACAAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
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                                                                                                                                                                                                                                                                                                                                                                                                             1 MetGlyTrpArgTrpIlePheLeuPheLeuLeuSerGlyThrAlaGlyValGlnCysGln 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCGCCAGATGCCC
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 17, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Straubberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, BC003078; AAH03878.1; -.
HSSP; P01842; FRBL
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_like.
InterPro; IPR003060; Ig_MHC.
InterPro; IPR00396; Ig_v.
Pfam; PF00047; ig; 3.
EMBL; BC013490; AAH13490.1; -.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 481 AA; 52105 MW; 970PF6BDIS9463F65 CRC64;
                                                                                                                                                                      481
80
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Matches:
Conservative:
Mismatches:
Indels:
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427.00
72.11%
54.42%
50.47%
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Best Local Similarity:
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61 GIGCAGCIGGIGCAGICIGGAGCAGAGGIGAAAAAGCCCGGGGAGICTCIGAAGAICTCC 120
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                                                                                                                                                                                                                                                                                                                                                                 181 GGGAAAGGCCTGGAGTGGATGGGGATCATCTTATCCTGGTGACTCTGATACCACATACAGC 240
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101 GlnLeuSerSerLeuThrSerGluAspSerAlaValTyrTyrCysThrArgGlyTyrGly 120
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|MetGlyTrpAsnCysIleIleLeuPheLeuValAlaThrAlaThrGlyValHisSerGln 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP) ";
Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; A8069915; BAB63931.1;
InterPro; IPR003006; Ig_MHC.
Pfam: PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C99D2433F2BAD8A0 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                          Conservative:
Mismatches:
Indels:
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                    Percent Similarity:
Best Local Similarity:
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (protein for MGC:18977)
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Mu
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG like; 1.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC012207, AAM12207.1;
InterPro; IPR003006; Ig_MHC.
PFam; PF00047; ig; 2.
SEQUENCE 278 AA; 29778 WW; F894F955DDCD948A CRC64;
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                                  TCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTCTGGA
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Bohlen H., Diehl V., Wolf J.;

"Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a patient with mixed cellularity Hodgkin's disease is associated with somatic mutations within the untranslated regions of rearranged and class switch recombinated Ig genes.";

Submitted (ApR-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AJOOSS70; CAA06599.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;
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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
SMART. SMO0406; IGv; 1.
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TISSUE=PERIPHERAL BLOOD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 AGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTAC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 CTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGAGACCAA 357
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                                                                                                            58 GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAGCCCGGGGAGTCTCTGAAGATC 117
                                                                                                                                                                                                                               118 TCCTGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCGCCAGATG 177
                                                                                                                                              21 SerCysLysAlaSerGlyTyrThrPheThrSerTyrTrpIleThrTrpValLysGlnArg 40
                                                                                                                                                                                                                                                                                                                                                                                    415 ACCAAGGCCCCATCGGTCTTCCCCCTG------GCACCCTCCTCCAAGAAG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 CTGGGCCTC---TTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Strausberg R.;

L Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; RC003888; AAH03888.1; -.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003500; Ig_like.

R InterPro; IPR003500; Ig_like.

R InterPro; IPR003506; Ig_WHC.

R InterPro; IPR003506; Ig_WHC.

R InterPro; IPR003506; Ig_WHC.

R SMART; SM00407; ig; 3.

R SMART; SM00407; IGcl; 3.

DR SWART; SM00406; IG like; 1.

DR SWART; SM00410; IG like; 1.

DR SWART; SW00410; IG like; 1.

DR SWART; SW00410; IG like; 1.

DR SWART; SW00410; IG like; 1.

DR SWART; SW00410; IG like; 1.

SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
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81
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
Mus musculus (Mouse).
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Matches:
Conservative:
Mismatches:
Indels:
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                                                 US-08-728-463B-207 (1-462) x Q924Q0 (1-143)
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417.50
70.20%
53.64%
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139 AGCITITACCGGCTACTGGATCGGCTGCGCCAGATGCCCCGGGAAAGGCCTGGAGTGG 198
              CTCGCCCTCCTCCTGGCTGTTCTCCAAGGAGTCTGTGCCGAGGTGCAGCTGGTGCAGTCT
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                                                             88 GTGAAAAAGCCCGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTACC 147
                                                                                                    148 GGCTACTGGATCGGCTGGGTGCCCAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGGATC 207
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90 ThrArgasnThrSerThrThrThrValTyrMetGluLeuSerArgLeuArgPheGluAsp 109
                                                                                                                                             208 ATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCAGGTCACCATC 267
                                                                                                                                                                                                                                          268 TCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCGTGAAGGCCTCGGAC 327
                                                                                                                                                                                                                                                                                 TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACAAGGCCCCATCGGTCTTC 435
                                              29
                                                                                      49
                                                                                                                  87
                                                                                                                                                              70 IleGlyProGlyValGlySerThrMetCysAlaGluLysPheGlnGlyArgLeuThrMet 89
                                  CTCCTGGCTGTTCTCCAAGGAGTCTGTGCCGAGGTGCAGCTGGTGCAGTCTGGAGCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
InterPro; IPRO00005; HTMARAC.
InterPro; IPRO00005; IQ_C2.
INTERPRO; IPRO00005; IQ_MHC.
R PROSITE; SW00408; IGC2; 2.
R PROSITE; PS00299; IG MHC; UNKNOWN_3.
R PROSITE; PS00299; IG MHC; UNKNOWN_3.
M Immunoglobulin domain.
SEQUENCE 614 AA; 67921 MM; SSEFS36E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butel:
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                 Q96GA6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (protein for MGC:15420).
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78
26
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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 US-08-728-463B-207 (1-462) x 095978 (1-157)
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                                                                                                                                                                                                                                                                                                              CCCCTGGCACCCTCCTCCAAG 456
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411.00
71.72%
53.79%
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TISSUE=B-CELL;
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318
                                             199 ATGGGGATCATCTATCCTGGTGACTCTGATACCACATACAGCCCGTCCTTCCAAGGCCAG 258
                                                                                                                                          319 GCCTCGGACACCGCCATGTATTACTGTGCGAGAGACCAACTGGGC------CTC 366
                                                                                                                                                                                                                TITGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGTCAGCCTCCAAGGGCCCA 426
                                                                                                                                                                                                                                                                                    99
                                                                                           86
47 ThrPheThrTyrArgTyrLeuHisTrpValArgGlnAlaProGlyGlnAlaLeuGluTrp
                                                                    259 GICACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDILINE-98277139; PubMed-9614934;
ML X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.,
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metasoa; Chordata; Craniata; Vertebrata; Euteli
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
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78
18
18
13
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035022; AAD56258.1; -.
HSSP: PO1772; 2FB4.
InterPro; IPRO3006; Ig_MHC.
InterPro; IPRO3306; Ig_V.
Pfan; PF00047; 1g; 1.
SYART; SM00406; IGv; 1.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                    427 TCGGTCTTCCCCCTG 441
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410.50
75.59%
61.42%
48.52%
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Homo sapiens (Human)
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Query Match:
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118 recremangeerrerganneagerrenacegeracegaregargegecagang 177
                                                                                                       298 CTGCAGTGGAGCGTGAAGGCCTCGGACACGCCATGTATTACTGTGCGAGAGACCAA 357
                                                                                                                                 238 AGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTAC 297
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99 ---GlyLeuTyrValValValProAlaAlaPheSerArgPheAspTyrTrpGlyGlnGly_117
                                 388 ACCCTGGTCACCGTCTCCTCA 408
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SUMMARIES

Human immunoglobul Amino acid sequenc Anti-murine CTLA-4 Human leukocyte an Human leukocyte an

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Human novel protein #48.
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4120.219 Million cell updates/sec
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                             3, 2003, 08:56:21 ; Search time 29.8828 Seconds
version 5.1.6
- 2003 Compugen Ltd
                   - protein search, using frame_plus_n2p model
                                                                                                           hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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, Ygapext
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GenCore
Copyright (c) 1993
                                               US-08-728-463B-207
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length: 2000000000
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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Maximum DB seq
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Human Ab heavy cha Amino acid sequenc Human leukocyte an Human leukosyte an Dig1 antibody heav Amino acid sequenc Human monoclonal a Antibody AAL 160 h Sequence of the VH Monoclonal antibod Monoclonal antibod Human BLyS binding Chimeric SCBP CGML Chimeric SCBP CGML Chimeric SCBP CGML Chimeric SCBP CGML Chimeric SCBP CGML Chimeric SCBP CGML Chimeric SCBP CGML

AAR54050

AAW24987

AA015186

ABP45301 AAE20408 AAE20409

AAE20410

Amino acid sequenc Amino acid sequenc Amino acid sequenc Anti-Interleukin-1

AAY56708 AAY56709

AAU75161 AAU76521

AAE20407

d 5G1.1 VH SCBP C6.5

Humanised

Chimeric

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anti-Fas HMFG-1 F

Humanised Humanised

Humanised Humanised

AAM52162 AAM52154

Humanised

immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder. Human; novel protein; Antianaemic; osteopathic; antiinflammatory; Humanised ALIGNMENTS AAM52163 AAM52166 AAM52155 AAM52168 AAU14177 standard; Protein; 474 AA 24-OCT-2001 (first entry)

Homo sapiens

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CAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGAGACCAACTG .360
                                                                                                                                                                           ----TITGACTACTGGGGCCAGGGAACCCTGGTC 396
                                                                                                                                                                                                     121 GlyThrAlaProSerTyrHisTyrTyrGlyLeuAspValTrpGlyArgGlyThrSerVal 140
                                                                                                                                                                                                                                      397 ACCGTCTCCTCAGCCTCCACCAAGGGCCCCATCGGTCTTCCCCCTGGCACCTCCTAAG 456
                                                                                                                                                                                                                                                         The present invention relates to novel human monoclonal antibodies. The antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II receptor, resulting in the inhibition of the signal transduction of human TGF-beta into cells. The antibodies can be used for the prevention and treatment of diseases associated with the production of TGF-beta, such as tissue fibrosis in the lung, liver, skin, kidney or other tissues, and atherosclerosis, atopy, keloid and arthritis. The present sequence was used in the present invention.
          61 AspLysGlyLeuAlaTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyrSer 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis; Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy; signal transduction inhibition; tissue fibrosis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human monoclonal antibodies recognizing human TGF-beta II receptor, useful for treating TGF-beta associated diseases such as tissue
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133
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                        AAB99113 standard; Protein; 146 AA.
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08-NOV-2000; 2000JP-0340216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein SEQ ID 8.
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-2001
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-2001
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                                                                                                                                                                                                                                                                                                                                     The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as colerant protein expression or activity. The polypeptides can be used as colerant protein expression or activity. The polypeptides can be used as colerant protein expression or activity. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense blA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Craise antibodies/elicit an immune response, to determine plantitative disorders, treatens markers, regenerating bone, cartiage, tendon, cligament and/or nerve tissue, wound healing, treating plants, promoting contraceptive, reating osteoporosis and osteoarthritis, anaemia, contraceptive, reating osteoporosis and osteoarthritis, anaemia, allorant in infection or from autolimunity, cancer, alloray, asthma, cungal infection or from autolimunity, cancer, alloray, asthma, crample of the present sequence represents a protein of the invention.
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                                                                                                                                                                             Tang YT, Liu C, Drmanac RT;
                                                                             25-JAN-2001; 2001WO-US02623
                                                                                                              25-JAN-2000; 2000US-0491404
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86.25%
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Best Local Similarity:
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N-PSDB; AAS22482
               WO200155437-A2.
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Homo sapiens
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                                      GGGAAAGGCCTGGAGTGGATTGATCTTATCCTGGTGACTCTGATACCACATACAGC
                                                                                                                          CCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTG
                                                         GTGCAGCTGGTGCAGTCTGGAGGTGAAAAAGCCCCGGGGAGTCTCTGAAGATCTCC
                                                                                                                                                                            CAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGA-----
                                                                                                                                                                                                                                                                                                                                         // immunoglobulin; interleukin 8; IL8; immunogen;
phage display library; immunisation; transgenic animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOS-) BIOSITE DIAGNOSTICS INC.
(GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
                                                                                                                                                                                                                                                                                                                          TRO005 HuMab Happa chain protein sequence 3E9H.
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              US-08-728-463B-207 (1-462) x AAB99113 (1-146)
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99US-0453234.
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human antibody pl
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Synthetic.
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01-DEC-1999;
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The present invention describes a method (MI) for producing a human antibody phage display library (I), comprising: (I) providing a nonhuman transpenic animal (II) whose genome comprises human immunoglobulin genes; (2) isolating nucleic acide encoding human antibody chains (III) from lymphatic cells; and (3) forming a library of display packages whose members comprise a nucleic acide encoding (III) which is displayed from the package. The method is used for producing a human antibody display library, e.g., a Fab phage display library. The display method may be used to screen nucleic acids encoding antibody chains obtained from immunised nonhuman transgenic animals, and from this a population of antibodies may be prepared. Production of a human monoclonal antibodies (immunise thumans with antigens, and the difficulties faced with immortalising B cells are avoided. AAH29958 to AAH30966 and AAB74094 to AAB75056 represent sequences used in the exemplification of the present invention.
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Best Local Similarity:
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AAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAG

418

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US-08-728-463B-207 (1-462) x AAB75052 (1-225)
                                                             Gray J,
                              99US-0157415.
99US-0453234.
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623.00
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89.47%
73.64%
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                                                                     WPI; 2001-335567/35.
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Best Local Similarity:
Query Match:
DB:
WO200125492-A1.
                              02-OCT-1999;
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Homo sapiens.
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01-DEC-1999;
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Matches:
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Mismatches:
Indels:
                             GENPHARM INT SUBSIDIARY OF MEDAREX INC.
                                                           Lonberg N;
                                                                                                                                                              Example 37; Page 122-123; 161pp; English.
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The present invention describes a method (MI) for producing a human antibody phage display library (I), comprising: (I) providing a nonhuman transgenic animal (II) whose genome comprises human immunoglobulin genes; (2) isolating nucleic acids encoding human antibody chains (III) from libraty cells, and (3) forming a library of display packages whose muchers comprise a nucleic acids encoding (III) which is displayed from the package. The method is used for producing a human antibody display library, e.g., a Fab phage display library. The display method may be used to streen nucleic acids encoding antibody chains obtained from immunised nonhuman transgenic animals, and from this a population of antibodies may be prepared. Production of a human monoclonal antibodies antibodies with antispens, and the difficulties faced with immortalising B cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056.
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Mismatches:
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                                                                                                                                                                                                                                                                                          TRO005 HuMab Happa chain protein sequence 3E3H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOS-) BIOSITE DIAGNOSTICS INC.
(GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lonberg N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 37; Page 122-123; 161pp; English.
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                                                                                                                                   AAB75053 standard; Protein; 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0157415.
99US-0453234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2000; 2000WO-US27237.
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73.64%
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biodiversity and for nutritional purposes. The present sequence protein of the invention.
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                                   128 AA
                                                                                        Percent Similarity:
Best Local Similarity:
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                                                        Alignment Scores:
Pred. No.:
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                                                                                                                                                                       CCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTATCCTGGTGACTCTGATACCACATAC 237
                                                                                                                AGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTAC 297
                                                                                                                                                           CTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGAGACCAA 357
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                                                                               SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr
GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle
                                                                                                                                                                                                       358 CTGGGCCTCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACC
                                     21 SerCysLysGlySerGlyTyrSerPheThrAsnTyrTrpIleGlyTrpValArgGlnMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                           Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
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                                                                                                                                                                                                                                                    418 AAGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAG 456
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Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                        Human EST encoded protein SEQ ID NO: 1521
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                                                                                                                                                                                                                                                                                                                      AAM23996 standard; Protein; 128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
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                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2001 (first entry)
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Cao Y, Drmanac RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complementarity determining region; antibody; primate; immunogenicity; Old World ape; Old World monkey; antigen-binding affinity.
                                                                                                                                                                                                                        TGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCGCCAGATGCCC
                                                                                                                                                                                                                                                                                                                                                                                                 41 CysLysGlySerGlyTyrSerPheThrSerTyrTrplleGlyTrpValArgGlnMetPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGAAAGGCCTGGAGTGGATCATCTATCCTGGTGACTCTGATACCACATACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTG
                                                                                                                                                                                                  ATGGGGTCAACCGCCATCCTCGCCCTCCTCCTGGCTGTTCTCCAAGGAGTCTGTGCCGAG
                                                                                                                                                                                                                                                                                                             21 ValGlnLeuValGlnSerGlyAlaGluValLysEvSProGlyGluSerLeuLysIleSer
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115
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    Length:
Matches:
Conservative:
Mismatches:
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1.19e-46
601.00
98.29$
98.29$
71.04$
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93WO-JP00603

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(NISB ) JAPAN TOBACCO INC.
                                             Honjo T, Matsuda F;
                                                              WPI; 1995-006791/01
                                                                           N-PSDB; AAQ78989
         10-MAY-1993;
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                The invention provides an antibody (Ab) comprising donor CDRs (complementarity determining regions) derived from a non-human antigenspecific donor antibody, and an acceptor framework from a non-human primate. The Abs are prepared by grafting CDRs from a non-human antigenspecific donor antibody onto homologous Old World ape or monkey acceptor frameworks. The Abs have reduced immunogenicity and are better tolerated in humans (because of the close similarity between the human and primate proteins), but retain the full antigen-binding affinity of the donor
                                                                                                                                                                                                                                                                    61 GTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAGCCCGGGGAGTCTCTGAAGATCTCC 120
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                                                                                                                                                                                                                                                                                                                                                          Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain; cosmid; placenta; vector; pJB81; E.coli; mammalian.
                                                                                                                                                                Conservative:
Mismatches:
Indels:
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                                                                                                                                              Length:
Matches:
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 Example 1; Page 46; 123pp; English
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                                                                                                                                                      601.00
88.49%
85.61%
71.04%
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                                                                                                                 Sequence 140 AA;
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Best Local Similarity:
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Pred. No.:
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Protein sequences (AAR66295-51) are novel human immunoglobulin heavy (halain sequences encoded by novel isolated genes. The genes constructs: V202; V103; V21; V6; V24; 3-31; M84; M118 and M111, by PCR emplification using primers AA078917-38. The genes are subdivided into 5 fragments were isolated from the genes are subdivided into 5 fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with TagI restriction enzyme. The fragments were located from high molecular weight DNA from human The fragments were separated by gel electrophoresis and 3-45 kb fractions were collected. The fragments were ligated with ClaI-digested cosmid were collected. The fragments were ligated with ClaI-digested cosmid into B.coli 490A. The fragments were then subcloned by colony hybridisation. The VN genes and the DNA fragments encoding them are useful in producing human immunoglobulin in mammalian hosts.
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DNA fragment comprising human immunoglobulin Vh genes production of human immunoglobulin in mammalian hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                               Claim 58; Page 96-97; 130pp; Japanese.
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98.29%
97.44%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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41 AspThrArgTyrSerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIle
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577.00
94.87%
92.31%
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                                                                                                                                                                                                                                                                                                                                             07-FEB-2000 (first entry)
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                          Human; immunoglobulin; Ig; transgenic; non-human mammal; inactivated endogenous Ig locus; B-cell development; U-H; D-H; V-H gene; kamman heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene; kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa; production; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 TCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGG 165
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Amino acid sequence of a human antibody fragment.
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                                                                                                                                                                                                                                                                                                                                           Klapholz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 74; 128pp; English.
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Mendez M;
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The present sequence is the anti-murine CTLA-4 sFv (M24 sFv). This is a membrane-associated protein which binds to CTLA-4. Chimeric constructs comprising DNA sequences encoding the extracellular domain of murine CTLA4 and human CDB were used for the study of anti-CTLA4-sFv protein. The anti-hCTLA4 sFv functions as a ligand binding to CTLA-4 on activated 1-colls and anteagonises the co-stimulatory signal provided by the interaction between donor B7 and recipient CD28. Cells expressing the anti-hCTLA4 sFv failed to stimulate T-cell proliferation. This is used in
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                                   AGCACCGCCTACCTGCAGTGGAGCCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGT
                                                                                                                                  346 GCGAGAGACCAACTGGGCCTCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC
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fragments are useful for the preparation of a pharmaceutical fitreatment of humans. They are also useful for HLA phenotyping.
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fragment specific for human leukocyte antigen CW6, useful for treatment
of humans and for human leukocyte antigen phenotyping .
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miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
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fragment specific for human leukocyte antigen Cw6, useful for treatment
of humans and for human leukocyte antigen phenotyping
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miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
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245 AA;
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                    are specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleotides. The specification describes a human immunoglobulin fragments specific for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are useful for the preparation of a pharmaceutical for the treatment of humans. They are also useful for HLA phenotyping.
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           AAB67617-23 represent single chain antibody (scFv) fragments which
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                               US-08-728-463B-207 (1-462) x AAB67621 (1-245)
                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW27555 standard; Protein; 120 AA.
                                                                                                                                                                      3.81e-44
574.00
93.22%
93.22%
67.85%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain; consensus.
                                                                                                                                         245 AA;
                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-1996;
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                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JAN-1998
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DB:
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                                                                                                                                                                         Pred. No.:
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81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgTrpGly 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 ProGlyLysGlyLeuGluTrpMetGlyIlelleTyrProGlyAspSerAspThrArgTyr
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    using synthetic
gene as universal

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                                                                                                                                                                                                                                                                 variable region synthetic sequence VH5, used in the preparation a human derived antibody gene library.
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Plueckthun
                                                                                                                                                                                                                                               chain
                                                                                                                                                                                                                                                                                                                                                                                                  120
110
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                                                                                                         Preparation of human derived antibody gene library consensus sequences, and signal consensus antibody framework for highly diverse antibody libraries
                                                                                                                                                                                                                                               The present sequence is the human antibody heavy
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Conservative:
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    Moroney
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                                                                                                                                                                                                                                                                                                                                                                                                     4.69e-44
  Knappik A,
                                                                                                                                                                                                                                                                                                                                                                                                                         572.50
91.67%
91.67%
67.67%
                                         1997-179277/16.
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Misc-difference 82
                                                                                                                                                                                                                                                                                                                                    120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity:
                                                                N-PSDB; AAT87953
  Ilag V,
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Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens,
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177

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297

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408

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101 LysGlyHisPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 117
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567.00
92.37%
92.37%
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                                                                                                                                                                                                                                                                                        (MORP-) MORPHOSYS AG.
                                                                                                                                                                                                                                                                                                                                    WPI; 2001-218451/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 AA;
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                                                                                                                                                                                                    WO200114558-A1.
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Homo sapiens.
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                                                                                                                                                                                                                        01-MAR-2001.
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DB:
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                                                                                                                                                                                                                                            firgment. The fragment is used to produce a mixture or panel of a different specific binding members, each comprising an antibody VH cand/or VL variable domain and capable, when displayed on the surface and/or VL variable domain and capable, when displayed on the surface of filamentous bacteriophage particles or in the case of a specific binding member comprising the DS VH and/or VL variable domain when bood brain barrier (BBB). The panel is useful for the selection of specific binding members with a desired property such as ability to bind endothelial cells or other brain cell antigen, ability to bind endothelial cells or other brain cell antigen, ability to bind intracellular adhesion molecules and to bind transferrin receptor. The antibodies are useful in diagnosis, prophylaxis and receptor. The national disease, AIDS-related dementia, epilepsy and transferrin disease, such as Alzheimer's disease, prion diseases involving inflammation cocurring within the brain or central nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 GAGGTGCAGCTGGAGCAGGCAGAGGTGAAAAAGCCCCGGGGAGTCTCTGAAGATC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 recreinagegriergearacageriracegecracigearegecregeregeceagare 177
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                                                                                                                                                                  Mixture or panel of antibodies for selecting specific binding members that cross the blood brain barrier, for use in delivering different molecules and treating neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SerCysLysGlySerGlyTyrSerPhrSerTyrTxpIleGlyTrpValArgGlnMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCGGGAAAGGCCTGGAGTGGATGGGATCATCTATCCTGGTGACTCTGATACCACATAC
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                                                                                                                                                                                                                                    The present sequence represents an antibody variable heavy chain (VH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGGCCTCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 408
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Matches:
Conservative:
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                                                                                                                Ward G, Miller K;
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                                                                                      (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                              Claim 1; Page 108; 109pp; English.
                                           27-NOV-2000; 2000WO-GB04501
                                                                   99US-0170599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.74e-44
569.00
93.16%
91.45%
67.26%
                                                                                                              Webster C, Osbourn J,
                                                                                                                                  WPI; 2001-398131/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA;
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                                                                                                                                              N-PSDB; AAH42410.
 WO200144300-A2.
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Best Local Similari
                                                                 13-DEC-1999;
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Pred. No.:
                       21-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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AAB67617-23 represent single chain antibody (scFv) fragments which are specific for human leukocyte antigen (HLA)-Cw6. The fragments are derived from a synthetic human combinatorial antibody library based on molecular consensus frameworks and CDRs randomised with trinucleocides. The specification describes a human immunoglobulin fragments specific for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in studies of natural killer cell silencing as well as miscarriages. HIA-Cw6 demonstrates a disequilibrium in some recurrent abortions. Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin fragments are useful for the preparation of a pharmaceutical for the treatment of humans. They are also useful for HLA phenotyping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 GAGGTGCAGCTGGTGCAGTCTGGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated human immunoglobulin or functional immunoglobulin
fragment specific for human leukocyte antigen Cw6, useful for treatment
of humans and for human leukocyte antigen phenotyping -
                                                                                                                                                                                                                               antigen; HLA; HLA-Cw6; natural killer cell silencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCGCCAGATG
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                                                                                                                                                                   Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_7.
                                                                                                                                                                                                                         Human leukocyte antigen; HLA; HLA-Cw6; natural Kıller cell sılen
miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
Conservative:
Mismatches:
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AAB67623 standard; Protein; 245
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Sequence 4, Appli
Sequence 4, Appli
Sequence 16, Appl
Sequence 16, Appl
Sequence 1995, Ap
Sequence 1995, Ap
Sequence 2088, Ap
Sequence 1997, Ap
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Sequence 2103, Ap
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                                                            Sequence 36, App
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Sequence 9, Appl:
                                                                                                                                                                         Sequence 42, Ap
Sequence 7, Appl
Sequence 7, App
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Sequence 55,
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                                                                                                                  Sequence 40,
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Sequence 6, Application US/10078958

Sequence 6, Application US/10078958

Sequence 6, Application US/10078958

Sequence 6, Application US/10078958

GENERAL INFORMATION:
APPLICANT: ACHERLAPATI, RAJU
APPLICANT: KLAPHOLZ, SUSAN
APPLICANT: MENDEZ, MICHAEL J.
APPLICANT: GREEN, LARRY
TITLE OF INVENTION: THEREFROM
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CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 08/759,620
PRIOR FILING DATE: 1996-12-03
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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; ORGANISM: Homo sapiens
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Command line parameters:
-MODEL=frame+ n2p, model - DEV=xlp
-MODEL=frame+ n2p, model - DEV=xlp
-G=Cgn2 1/USFTO_spool/US08728463/runat_03062003_085618_16959/app_query.fasta_1.3690
-G=Cgn2 1/USFTO_spool/US08728463/runat_030FTX=xrapb - MINMATCH=0.1
-DG=Ch2 1/DSPTIO_spool/USDSTIONS AA -QFFWT=fastan -SUFFIX=xrapb - MINMATCH=0.1
-LOOPCL=0 - LOOPEXT=0 - UNITS=bits -START=1 - SND=-1 - MATRIX=blosum62
-TRANS=human40.cdi - LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100
-THR MIN=0 - ALIGN=15 - MODE=LOCAL - OUTFWT=pct - NORM=ext - HEAPGTEE=500 - MINLEN=0
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1: /cgn2_6/ptodata/1/Pubpaa/USO8_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-10-125-687-6
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US-09-880-748-1537
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Listing first 45 summaries
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Xgapop 10.0 , Xgapext
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238 AGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACGGCTAC 297
                                                                                   APPLICANT: Luo, Peter
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
FILE REFERENCE: 26.050-705
CURRENT APPLICATION NUMBER: US/10/025,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 120
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                                                                                                                                                                                          ; Sequence 6, Application US/10025687
; Patent No. US20020142255A1
; GENERAL INFORMATION:
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81 AlaArgGlnAspGlyAspSerPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 100
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Publication No. US20030054407A1
GENERAL INFORMATION:
APPLICANT: Luo, Pecer
TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
CURRENT APPLICATION NUMBER: US/10/125,687
CURRENT FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 120
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| ApThrakgTyrSerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIle
                                                                                                                                           TYPE: PRT

OGGANISM: Artificial Sequence
FRATURE:
CTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-125-687-6
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572.50
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67.67%
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93.16%
92.31%
68.20%
          Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-10-125-687-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
FILE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/210,816
PRIOR APPLICATION NUMBER: 60/210,816
PRIOR APPLICATION NUMBER: 60/270,486
PRIOR FILING DATE: 2000-10-17
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 201-03-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN VET: 2.0
SSEC ID NO 1537
LENGTH: 252
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US-10-035-637-4

i Sequence 4, Application US/10035637

j Sequence 4, Application No. US20030031667A1

j GENERAL INFORMATION:
 j APPLICANT: Dec, Yashwant M.
 j APPLICANT: Reler, Tibor
 j TITLE OF INVENTION: CELLS
 j FILE REFERENCE: MXI-166CP
 j CURRENT APPLICATION NUMBER: US/10/035,637
 j CURRENT FILING DATE: 2001-11-07
 j PRIOR APPLICATION NUMBER: 09/851,614
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108
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Mismatches:
Indels:
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Matches:
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567.00
88.80%
86.40%
67.02%
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysThrArgGlyAsp 100
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; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; TIME REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT PLIANG DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-10-17
; PRIOR FILING DATE: 2000-10-17
; PRIOR PLING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR PLING DATE: 2001-03-21
; PRIOR PLING DATE: 2001-03-21
; PRIOR PLING DATE: 2001-03-21
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/203,126
PRIOR PILING DATE: 2000-05-08
PRIOR APPLICATION NUMBER: USSN 60/230,739
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 116
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558.50
93.16%
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CORGANISM: Homo sapiens
US-10-035-637-4
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ORGANISM: Homo sapiens
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US-09-880-748-1312
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358 CTGGGC----
                                           Percent Similarity:
Best Local Similarity:
Query Match:
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                  Alignment Scores:
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                                                                                                                                                                                                    394 GTCACCGTCTCCTCAGCCTCC------414
                                                                                                                                                                                                                                          OCCANION: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Human/murine
OTHER INFORMATION: chimeric single chain binding polypeptide (C6ML3-9
US-09-888-721-36
                                                                                           US-08-728-463B-207 (1-462) x US-09-880-748-1312 (1-249)
                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                       551.50
77.33%
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65.19%
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                                          Percent Similarity:
Best Local Similarity:
Query Match:
US-09-880-748-1312
                  Alignment Scores:
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LENGTH: 269
TYPE: PRT
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118 TCCTGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCGCCAGATG 177
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                                                                                                                                                                                                                                                                                                                                                                                        238 AGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACGGCCTAC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 CTGCAGTGGAGCAGCCTGAAGGCCTCGGACACGCCATGTATTACTGTGGGAGAGACCAA 357
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101 ValGlyTyrCysSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
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                                                                                                                                                                                                                                                                                                                                      141 GlyGlyGlySerGlnSerValLeuThrGlnProProSerVal---SerAlaAlaProGly 159
                                                                                                                                                               58 GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATC
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APPLICANT: Huston, James S.
APPLICANT: Wils, Pierre
APPLICANT: Zhu, Quan
APPLICANT: Laurent, Olivier
APPLICANT: Laurent, Olivier
APPLICANT: Scherman, Daniel
TITLE OF INVENTION: BICHORINERED VEHICLES FOR TARGETED NUCLEIC ACID
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 23611-A USA
CURRENT FILING DATE: 2001-06-23
CURRENT FILING DATE: 2000-06-23
PRIOR PLING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver: 2.0
SSOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
PRGANISM: Artificial Sequence
PEATURE:
OTHER INFORWATION: Description of Artificial Sequence:Human/murine
 269
106
106
30
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                         US-08-728-463B-207 (1-462) x US-09-888-721-36 (1-269)
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; Patent No. US20020132990A1
; GENERAL INFORMATION:
               530.00
71.60%
65.43%
62.65%
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| Patent No. US200201329901 |
| GENERAL INFORMATION: |
| APPLICANT: Huston, James S. |
| APPLICANT: Huston, James S. |
| APPLICANT: Huston, James S. |
| APPLICANT: Huston, James S. |
| APPLICANT: Advance C. |
| APPLICANT: Advance C. |
| APPLICANT: Scherman, Daniel |
| APPLICANT: Scherman, Daniel |
| TITLE OF INVENTION: BLIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVERY DELIVER
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; 'OTHER INFORMATION: chimeric single chain binding polypeptide; OTHER INFORMATION: (C6ML-3-9sFV'-L1-KDEL)
US-09-888-721-38
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Mismatches:
Indels:
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Best Local Similarity:
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Pred. No.:
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US-09-888-721-40
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Sequence 44, Application US/0988721

Sequence 44, Application US/0988721

GENERAL INCRMATION:

APPLICANT: Wils, Pierre

APPLICANT: Laurent, Olivier

APPLICANT: Laurent, Olivier

APPLICANT: Arassco, Wayne A.

APPLICANT: Acherman, Daniel

TITLE OF INVENTION: BICHORGINEERED VEHICLES FOR TARGETED NUCLEIC ACID

TITLE OF INVENTION: DELIVERY

FILE REFERENCE: 23611-A USA

CURRENT FILING DATE: 2000-06-25

PRIOR APPLICATION NUMBER: 60/213,653

PRIOR FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                       41 ProGlyLysGlyLeuGluTyrMetGlyLeulleTyrProGlyAspSerAspThrLysTyr
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                           Description of Artificial Sequence:Human/murine chimeric single chain binding polypeptide (C6ML3-9sFv'-L2-KDEL)
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Mismatches:
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Matches:
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ORGANISM: Artificial Sequence FEATURE:
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SOFTWARE: PatentIn Ver. 2.0
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                               OTHER INFORMATION:
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US-09-888-721-40
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Best Local Similarity:
Query Match:
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APPLICANT: Huston, James S.
APPLICANT: Wils, Pierre
APPLICANT: Zu, Quan
APPLICANT: Laurent, Olivier
APPLICANT: Laurent, Olivier
APPLICANT: ASTORMAND, Daniel
TITLE OF INVENTION: BIOENCINBERED VEHICLES FOR TARGETED NUCLEIC ACID
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 23611-A USA
CURRENT APPLICATION NUMBER: US/09/888,721
PRIOR APPLICATION NUMBER: 60/213,653
                                        FEATURE:
COTHER INFORMATION: Description of Artificial Sequence:Human/murine
OTHER INFORMATION: Chimeric single chain binding polypeptide
COTHER INFORMATION: (CGML3-98FV'-L2-nls)
                                                                                                                                                                                        US-08-728-463B-207 (1-462) x US-09-888-721-44 (1-291)
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Indels:
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Matches:
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Patent No. US20020132990A1
GENERAL INFORMATION:
SEQ ID NO 44
LENGTH: 291
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                   4.56e-35
530.00
71.60%
65.43%
62.65%
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Best Local Similarity:
Query Match:
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APPLICANT: Filpula, David R.
APPLICANT: Wang, Macliang
APPLICANT: Wang, Marc D.
TITLE OF INVENTION: No. US20020156248Alel Method for Targeted Delivery of Nucleic Ac FILE REFERENCE: 0977.2300003
CURRENT APPLICATION NUMBER: US/09/985,442
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/420,592
PRIOR FILING DATE: 1999-10-19
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                                                                                                                                      Description of Artificial Sequence:Human/murine chimeric single chain binding polypeptide (C6ML3-98Fv'-L2-H14)
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Matches:
Conservative:
Mismatches:
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Patent No. US20020156248A1
GENERAL INFORMATION:
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                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description
OTHER INFORMATION: chimeric si
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530.00
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62.65%
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
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US-09-888-721-42
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Best Local Similarity:
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                                               SEQ ID NO 42
LENGTH: 296
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APPLICANT: Wils, Pierre
APPLICANT: Wils, Pierre
APPLICANT: Laurent, Olivier
APPLICANT: Laurent, Olivier
APPLICANT: Laurent, Olivier
APPLICANT: Scherman, Daniel
TITLE OF INVENTION: BLOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 23611-A USA
CURRENT APPLICATION NUMBER: US/99/888,721
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/213,653
PRIOR APPLICATION NUMBER: 60/213,653
     ; LENGTH: 282; TYPE: PRT; ORGANISM: Artificial Sequence; FEATURE: FEATURE: , OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sFv US-09-983-580-7
                                                                                                                                                                                                                                                                                                  58 GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCT
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. US20020132990A1
GENERAL INFORMATION:
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270 SerLysLysLysLys 275
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 255
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                         7.97e-35
527.00
77.40%
68.49%
62.29%
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Best Local Similarity:
Query Match:
DB:
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; Sequence 7, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Macliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020151061A1e1 Method for Targeted Delivery of Nucleic Aci;
; TITLE OF INVENTION: No. US20020151061A1e1 Method for Targeted Delivery of Nucleic Aci;
; TILLE OF INVENTION: NO. US20020151061A1e1 Method for Targeted Delivery of Nucleic Aci;
; TILLE OF INVENTION: NO. US20020151061A1e1 Method for Targeted Delivery of Nucleic Aci;
; FILE REFERENCE: 0977.2300002
; CURRENT FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
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Matches:
Conservative:
Mismatches:
Indels:
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PRÍOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 282
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                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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OTHER INFORMATION: Humanised HMFG1
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                                                                                                                                                                                                                                                                                                           CTGGGC-----CTCTTTGACTACTGGGGC
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                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                    US-08-728-463B-207 (1-462) x US-09-888-721-34 (1-255)
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US-09-825-012-66

i Sequence 66, Application US/09825012

Patent No. US20020122798A1

GENERAL INFORMATION:

APPLICANT: Young, Robert

TITLE OF INVENTION: Compounds for Targeting
FILE REFERENCE: 43191-256808

CURRENT PAPPLICATION NUMBER: US/09/825,012

FRICH APPLICATION NUMBER: US 60/237,159

PRIOR PILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: US 60/237,159

PRIOR APPLICATION NUMBER: GB 0008049.9

PRIOR FILING DATE: 2000-04-03

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PatentIn version 3.1

SEQ ID NO 66

"LENGTH: 515
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ORGANISM: Artificial Sequence
FEATURE:
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160 GlnLys 161
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                                                                                                                                     1 ATGGGGTCAACCGCCATCCTCGCCTCCTGGCTGTTCTCCAAGGAGTCTGTGCCGAG 60
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| MetGlyTrpSerCysIleIleLeuPheLeuValAlaThralaThrGlyValHisSerGln
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Length:
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Conservative:
Mismatches:
Indels:
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523.50
79.74%
64.05%
                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Sequence 133, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Honjo, Tukuu APPLICANT: Honjo, Tukuu APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
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SOFTWARE: FASTSEN Windows95
SOFTWARE: FASTSEN FOR WINDOWS95
SOFTWARE: FASTSEN FOR WINDOWS95
SOFTWARE: PASTSEN FOR WINDOWS VERSION 2.0
CURRENT APPLICATION NAMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INPORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 29,066
TELECOMMUNICATION:
TELEPHONE: 617-542-5070
US-08-476-349A-81

US-08-665-202-44

US-08-665-202-53

US-08-665-202-59

US-08-458-516-22

US-08-458-516-23

US-08-458-516-13

US-08-458-516-13

US-08-665-202-46

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US-08-933-607-31

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US-09-027-449-52

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   STREET: 225 Fr.
CITY: Boston
STATE: MA
   200154
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2585.294 Million cell updates/sec
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                                                                                                                                                                                               1 ATGGGGTCAACCGCCATCCT......CACCCTCCTCCAAGAAGCTT 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                        June 3, 2003, 09:02:35; Search time 10.5159 Seconds
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6: /cgn2_6/ptOdata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                           OM nucleic - protein search, using frame_plus_n2p model
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US-09-025-769B-26
US-09-025-769B-67
US-09-025-769B-67
US-08-259-372A-8
US-08-468-671-8
US-08-665-202-5
US-08-665-202-5
US-09-069-821-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-665-202-33
US-08-665-202-33
US-08-478-039-81
                                                                                                                                                                                                                                                                                                                       262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                              0.5
7.0
7.0
                                                                                                                                                                                                                                         Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                  US-08-728-463B-207
                                                                                                                                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
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Match Length DB
                                                                                                                                                                                                                              BLOSUM62
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Database :

Result Š.

Total number of

Searched:

Perfect score:

Run on:

Sequence:

Scoring table:

Minimum DB seq Maximum DB seq

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178
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DB:
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                                                                                                                                                                                                                                                                                                  GIGCAGCIGGAGTCIGGAGCAGAGGTGAAAAAAGCCCGGGGAGICTCTGAAGAICTCC 120
                                                                                                                                                                                                                                                                                                                                                     121 TGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCGCCAGATGCCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                    240
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                                                                                                                                                                                                                                                                                                                                                                      61 GlyLygGlyLeuGluTrpMetGly1leileTyrProGlyAspSerAspThrArgTyrSer 80
                                                                                                                                                                                                                                                                                                                                                                                                          GGGAAAGGCCTGGAGTGGATGATCATCTATCCTGGTGACTCTGATACCACATACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACGGCCTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGTGGAGCAGCCTCGGACACCGCCATGTATTACTGTGCGAGA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: James F. Haley, Jr., Esq. c/o Fish \kappa Neave 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
FILING DATE: 18-MG-1998
FILING DATE: 18-MG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Knappik, Achim
APPLICANT: Fack, Peter
APPLICANT: 11ag, vic
APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Pluckthun, Andreas
APPLICANT: Pluckthun, Andreas
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                US-08-728-463B-207 (1-462) x US-08-545-809A-133 (1-117)
                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Application US/09025769B Patent No. 6300064 GENERAL INFORMATION:
     133:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                4.27e-51
598.00
98.29%
97.44%
INFORMATION FOR SEQ ID NO: SEQUENCE CHRAACTERISTICS: LENGTH: 117 amino acids TYPE: amino acid
                                                   TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-545-809A-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1251 Ave
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-025-769B-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                   61
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118 TCCTGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCGCCAGATG 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 CTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGAGACCAA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 CIGGGC-----CICITIGACIACTGGGGCCAGGGAACCCTGGTCACCGICTCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||||
99 LeuGlyGlyGlyGlyTyrTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCGGGAAAGGCCTGGAGGATGGGGATCATCTATCTGGTGACTCTGATACCACATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Nappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREE: James F. Haley, Jr., Esq. c/o Fish & Neave CITE: 1251 Avenue of the Americas STATE: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                          119
112
0
3
6
6
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 2,794
REFERENCE/DOCKET NUMBER: MORPHO/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
TELEFAX: (212)596-9000
TELEFAX: (112)596-9000
ELEFAX: (112)56-9000
TELEFAX: (112)56-9000
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                                                                                                                                                                                                                                                                                                                                                                  6.27e-49
576.00
92.56%
92.56%
68.09%
                                                                                                                                                                                                                                                          the TOPOLOGY: linear to MOLECULE TYPE: protein US-09-025-769B-26
                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406 TCA 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-025-769B-40
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98

6

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MEDITAL TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENT SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT IRFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS: ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-728-463B-207 (1-462) x US-09-025-769B-67 (1-120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
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Patent No. 5565354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 120 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                     ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-09-025-769B-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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US-08-259-372A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrplleGlyTrpValArqGlnMet 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-MG-1995
ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKT NUMBER: WORPHO/5
FILEMPONANTION E: (212)596-9000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ATRANDENESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-728-463B-207 (1-462) x US-09-025-769B-40 (1-120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 67, Application US/09025769B Patent No. 6300064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.39e-48
572.50
91.67%
91.67%
67.67%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-40
                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Knappik,
APPLICANT: Back, PR
APPLICANT: Ilag, V
APPLICANT: Ge, Lim
APPLICANT: Moroney,
APPLICANT: Placket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-09-025-769B-67
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Pred. No.:
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81 LeuGinTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgTrpGly 100
GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATC 117
                                                                                                                                                      118 TCCTGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCGCCAGATG 177
                                                                                                                                                                                                                                                                                                            178 CCCGGGAAAGGCCTGGAGGGATGGGATCATCTATCCTGGTGACTCTGATACCACATAC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTAC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGA----- 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
                                        1 GluValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLyslle 20
                                                                                                                                                                                                  21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40
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GGGAAAGGCCTGGAGTGGATGGGGATCATCTATCCTGGTGACTCTGATACCACATACAGC 240
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                                                                                                                                                                                                    CAGTGGAGCAGCCTGGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGAGACCAA--- 357
                                                                                                                                                                                                                                                                                                    101 GİnTrpArgSerLeuLyaAlaSerAspThrAlaMetTyrTyrCysAlaArgH1sValArg 120
                                                                                                                                                                                                                                                                                                                                                                         358 ......CTGGGCCTCTTTGACTACTGGGGCCAGGGA 387
                        61 GlyLysGlyLeuGluTrpMetGlyArgLeuAspProSerAlaSerSerAlaIlePheSer 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08468671
Patent No. 5648077
GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
CORPUTARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
FILING DATE: 06-JUN-1995
FILING DATE: "^^ATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10S 06/904,517
APPLICATION NUMBER: 0.5-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-UIN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION NUMBER: US 06/925,196
APPLICATION NUMBER: US 06/925,196
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PRODUCTION OF HUMAN MONOCLONAL
ANTIBODIES SPECIFIC FOR HEFATITIS B SURFACE ANTIGEN
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109
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
FILING DATE: 14-JUN-1994
CLASSIFICATION: 424
                                                                                  NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
APPLICATION NUMBER: US 07/676,036
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-UNN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1966
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1966
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: US 06/904,517
FILING DATE: US 05-85P-1966
ATTORNEY/AGENT INFORMATION:
NAME: Smith william M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          553.50
78.23%
74.15%
65.43%
                                                                                                                                                                                                                                   ZIP: 94111-3834
COMPUTER READABLE FORM:
GENERAL INFORMATION:
APPLICANT: Ostberg,
TITLE OF INVENTION:
TITLE OF INVENTION:
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CCCGGGAAAGGCCTGGAGTGGATGGGATCATCTATCCTGGTGACTCTGATACCACATAC 237
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                                                                                                                                                                                                                           GAGGTGCAGCTGCTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATC
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                                                                                                                                                                                                                                                                                            TCCTGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCGCCAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
      ; OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sFv
US-09-420-592A-7
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                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                         US-08-728-463B-207 (1-462) x US-09-420-592A-7 (1-282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202 FILING DATE: 13-UN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-665-202-5; Sequence 5, Application US/08665202; Patent No. 5977322; GENERAL INFORMATION:
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                                                                   5.29e-44
527.00
77.40%
68.49%
62.29%
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CITY: San Francisco
STATE: California
                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                         Alignment Scores:
Pred. No.:
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Sequence 7, Application US/09420592A;
Patent No. 6333396
GENERAL INFORMATION:
APPLICANT: Filpula, David R.
APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. 6333396el Method for Targeted Delivery of Nucleic Acids
FILE REFERENCE: 0977.2300001
FILE REFERENCE: 0977.2300001
CURRENT APPLICATION NUMBER: 06/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GluLysSerMetValGlnGlyValIleIleLysAspAlaPheAspIleTrpGlyGlnGly 140
                                                                                                                                                                                                                                                                                                                                                                                                            GTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCCGGGGAGTCTCTGAAGATCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCGCCAGATGCCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 CCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                             40
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109
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Mismatches:
Indels:
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                                                                                                                                                                                         Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 ACCCTGGTCACCGTCTCCTCA 408
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                         .09e-46
                                                                                                                                                                                                       553.50
78.23%
74.15%
65.43%
                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-09-420-592A-7
                                                                                                                                       US-08-468-671-8
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TITLE OF INVENTION: SINCLE-CHAIN ANTIGEN-BINDING PROTEINS
TITLE OF INVENTION: SINCLE-CHAIN ANTIGEN-BINDING PROTEINS
TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF WINDRESCEE: STERNE, SESSLER, GOLDSTEIN & POX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 TCCTGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCGCCAGATG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 CCCGGGAAAGGCCTGGAGTGGAATCATCTATCTGGTGACTCTGATACCATAC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 AGCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAGTCCATCAGCACCGCCTAC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATC
                                                                                                                                                                                                                                                        CUMPUTER READABLE FORM:

MEDLUM TYPES: Floppy disk

MEDLUM TYPES: Floppy disk

COMPUTER: IBW PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,821

FLING DATE: 30-ARR-1998

CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/067,341

FILING DATE: 02-DEC-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/063,074

FILING DATE: 23-OLD-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/063,472

FILING DATE: 33-OLD-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,449

FILING DATE: 33-OLP-1997

ATTORNEY ARENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0977.2280003

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
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523.00
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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74.24%
61.82%
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TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE;
US-09-069-821-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 AGCCCGTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACGCCTAC 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 GlyGlyGlySerGlnSerValLeuThrGlnProProSerVal---SerAlaAlaProGly 159
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                  RECISTRATION NUMBER: 38,498
RECISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 CAGGGAACCCIGGICACCGICTCCTCAGCCTCC--
                       FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
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Sequence 4, Application US/09069821
Patent No. 6233322
GENERAL INFORMATION:
APPLICANT: FILPULA, DAVID
APPLICANT: SHORK, ROBERT
APPLICANT: SHORK,
                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-665-202-5
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Best Local Similarity:
Query Match:
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                                                                                                                                                      <u> AGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTAC</u>
                                                           TCCTGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCGCCAGATG
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Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
TITLE OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.30
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Two Embarcadero Center, Eighth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                            382 CAGGGAACCCTGGTCACCGTCTCTCA 408
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APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UUN-1995
FILING PAPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UNN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HULLEY, TOM
REGISTRATION NUMBER: 38,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Parentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
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COMPUTER REDABLE FORM:
MEDIUM TYPE: Flore
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CITY: San Francisco
STATE: California
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                                                           190 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 209
                                       298 CTGCAGTGGAGCCAGCCTCGGACACCCCCATGTATTACTGTGGGAGAGACCAA 357
                                                                                                                  ----CTCTTTGACTACTGGGGC 381
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE CANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPEDINDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PR PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
                                                                                                                                                                                           382 CAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACC 417
                                                                                                                                                                                                                               250 GinGiyThrLeuValThrValSerSerAsnLysThr 261
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Mismatches:
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Matches:
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APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UNN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                    Sequence 32, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
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REGISTRATION NUMBER: 38,498
REFERENCE/DOCKEI NUMBER: 02307
TELECOMMUNICATION INPORMATION:
TELEPANE: (415) 576-0200
TELEPAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                358 CTGGGC-----
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COUNTRY:
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CURRENT APPLICATION DATA: NANDED: CANADED: NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADDICTANT NADOR NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NADOL NA
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POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH5 consensus
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
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GENERAL INFORMATION:
                          REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acide
TYPE: amino acide
TYPE: amino acide
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ORIGINAL SOURCE:
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Best Local Similarity:
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Fatent No. 5681722
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNAS ODONE, SWECKER & MATHIS
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                         US-08-728-463B-207 (1-462) x US-08-665-202-33 (1-98)
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APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION NUMBER: US 07/912,292
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY AGENT INFORMATION:
NAME: CALL-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Teskin Esq., Robin L. REGIGTRATION NUMBER: 35,030
                                                                                                      4e-43
                                                                                                                                513.00
97.96%
97.96%
60.64%
                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                           Alignment Scores:
Pred. No.:
US-08-665-202-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-478-039-81
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AGCCCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTAC 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 CTGGGC-----CTCTTTGACTACTGGGCC 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 TCCTGTAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCGCCAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCCGGGGAGTCTCTGAAGATC
                                                                                                                                                 COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOCTAME: BATENIN PC-DOS/MS-DOS
SOCTAMES PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-UN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HUNTEY: TOM
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Matches:
Conservative:
Mismatches:
Indels:
SSE: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
San.Prancisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-728-463B-207 (1-462) x US-08-665-202-44 (1-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 CAGGGAACCCTGGTC 396
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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83.20%
74.40%
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                                                             California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 CCCGGGAAAGGCCTGGAGTGGATGGGGATCATCTATCCTGGTGACTCTGATACCACATAC 237
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APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
WUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 CTGCAGTGGAGCCTGAAGGCCTCGGACACCCCCATGTATTACTGTGCGAGA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArg 98
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Matches:
Conservative:
Mismatches:
Indels:
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                                   FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: TEAKIN ENG. ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH5 consensus
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 44, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 703-836-2021
INFORMATION FOR SEQ 1D NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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508.00
96.94%
96.94%
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Best Local Similarity:
Query Match:
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Job time : 13.5159 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 CCCGGGAAAGGCCTGGAGGGATGGGGATCATCTATCTGGTGACTCTGATACCACATAC 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marks, James D.
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tunor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-728-463B-207 (1-462) x US-08-665-202-53 (1-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0208
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 13-JUN-1996
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-665-202-53
; Sequence 53, Application US/08665202
Patent No. 5977322
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 125 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501.00
82.40%
75.20%
59.22%
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hunter, Tom
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-53
                                                                                                                                                                                                                                     California
                                                                                                                                                                                                                                                                       94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
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298 CTGCAGTGGAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGGGAGAGACCAA 357
                                                   -----CTCTTTGACTACTGGGGC 381
61 SerProSerPheGlnGlyGlnValThrileSerAlaAspGluSerIleSerThrAlaTyr 80
                                                                                                                                      382 CAGGGAACCCTGGTC 396
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Perfect score:

Run on:

Sequence:

Scoring table:

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C;Accession: A49134; A:A: Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, J.J Clin. Exp. Immunol. 91, 506-509, 1993
A;Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in light A;Reference number: A49134; MUID:93185310; PMID:7680298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGATGTGACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGGAGACAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. IysCysAspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA; protein
A;Molecule type: mRNA; protein
A;Molecule type: mRNA;
A;Molecule type: mRNA;
A;Moss-references: BMBL:X67322; NID:g33268; PIDN:CAA47736.1; PID:g33269
A;Cross-references: EMBL:X67322; NID:g33269; EX;Note: sequence extracted from NCBI backbone (NCBIP:127088)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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                                                                                                                                     S52793
KIHUWK
S40317
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S40318
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S14237
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S24206
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S41814
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-MODEL=frame+ n2p model -DEV=xlp
-Q=/Cqn2 1/USPTO_spool/US08728463/runat_03062003_085615_16827/app_query.fasta_1.3690
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-ICPU=3
-NO MAAP -LARGEGUERY -NGG-SCORES=0 -WAIT -DSPBICOK=100 -LONGIGG
-DEV TYMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -KGAPEXT=0 -KGAPEXT=0.5 -FGAPEXT=0
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                                                                                                                                                                                                1 ATGGACATGGAGTTCCCCGT...........CCCGCCATCTGATGAAGCTT 439
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Copyright (c) 1993 - 2003 Compugen Ltd
                                                                           OM nucleic - protein search, using frame_plus_n2p model
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Maximum Match 100%
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1: pir1:*
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Database :

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Result No.

Qy 304 CCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATTACCCGTACACTTTTGGC 363	Alignment Scores: Pred. No.: Score:	21 121 41 181 61 241 81	Oy 301 CAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCG 351
121 GTCACCATCACTTGTCGGGCGAGTCAGCGTTTAGCAGCTGGTTAGCCTGGTATCAGCAG 180 11 1	aplens (man) 94 #sequenc_revision 26-May-1995 #t. 95 #sequenc_revision 26-May-1995 #t. 10	Score	1 I %

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CyAccession: A01881 #sequence_revision 31-Mar-1981 #text_change 24-Sep-1999
CyAccession: A01881 #sequence_revision genes - DNA sequences of two V-kappa generaly Reference number: A93241; MUID:81098966; PMID:6779204
A;Reference number: A93241; MUID:81098966; PMID:6779204
A;Redecule type: DNA
A;Residues: 1-117 *cBRN1>
A;Residues: 1-117 *cBRN1>
A;Residues: 1-117 *cBRN1>
A;Coss-references: GB:V00558; GB:J00244; GB:J00246; NID:g33176; PIDN:CAA23824.1; PID:g3
A;Coss-references: GB:V00558; GB:J00244; GB:J00246; NID:g33176; PIDN:CAA23824.1; PID:g3
A;Title: Exolution of immunoglobulin V genes: evidence indicating that recently duplicat
A;Reference number: A21056; MUID:83129397; PMID:6402305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaptain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l'Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer
                                                                                                                                                                                                                                                                                                                                                                                                  82 GlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnProAspAspPhe 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAACTTATTACTGCCAACAGTATGATAGTTACCCGTACACTTTTGGCCAGGGGACCAAG 375
                                                                                                                                                                                                CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAAAGCC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F.1-22/Domain: signal sequence #status predicted <SIG>P.22-117/Product: Ig kappa chain V-I region (HK101) #status predicted <MAT>F;38-112/Domain: immunoglobulin homology <IMM>F;45-110/Disulfide bonds: #status predicted
                                               2 ProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAlaLysCysAspIleGln
                                                                                                                                                                                                                                                                                                                                                                         GGCAGTGGATCTGGGATTTCACTCTCACCATCAGGAGCCTGCAGCCTGAAGATTTT
                                                                                                              ATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGT
                                                                                                                                       CCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGC
                                                                                                                                                                                                                           CCCGTTCAGCTCCTGGGGCTCCTGCTGTTTCCCCAGGTGCCAGATGTGACATCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-117 <BEN2>
A;Cross-references: GB:K01322; NID:g185993; PIDN:AAA58930.1; PID:g185994
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C;Species: Homo sapiens (man)
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A,Cross-references: GDB:136264
A,Map position: 2p12-2p12
A;Introns: 19/1
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40333
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S4033
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 < KLE>
A;Cross-references: ENBL:X72443; NID:9441354; PIDN:CAA51111.1; PID:9441355
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology < MM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 TGTGACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGGAGACAGAGTC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 TCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 CCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGTACACTTTTGGC 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 CCAGAGAAAGCCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGGTCCCA
                  A;Residues: 1-13z <albox.hrp.
A;Cross-references: EMBL:X72444
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>
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Best Local Similarity;
Molecule type: mRNA
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Pred. No.:
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Query Match

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Ly Aspace custure, numental cyspecies; Homo sapiens (man)
C;Species; Homo sapiens (man)
C;Species; Homo sapiens
C;Species; Homo sapiens
C;Accession: S40316
R;KLein, R.; Jaentchen, R.; Zachau, H.G.
R;KLein, R.; Jaentchen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 193
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Retaus: preliminary; translation not shown
A;Accession: S40316
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Coss-references: EMBL:X72426
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin homology <IMM>
142 AGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAGCCCCTAAG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LeuLeulleTyrHisIleSerSerLeuGlnThrGlyValProSerArgPheSerGlySer 80
                                       GCAACTIATTACTGCCAACAGTATGATAGTTACCCGGTACACTTTTGGCCAGGGGACCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 CAGCICCIGGGGCTCCTGCTGCTGTTCCCAGGTGCCAGATGTGACATCCAGATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 TATTACTGCCAACAGTATGATAGTTACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAG
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Cispecties: Homo sapiens (man)
Cibate: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Cispecties: $40.58 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Cispection: $40.58 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: $40312; MUID:94080891; PMID:8258341
A/Accession: $40368
A/Status: preliminary; translation not shown
                                            61 AGATGTGACATCCAGATGACCAGGTCTCCATCCTCACTGTCTGCATCTGTAGGAGACAGA
                                                                                               GTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAG
                          1 ATGGACATGGAGTTCCCCGGTTCAGCTCCTGGGGGCTCCTGCTGCTTTTCCCAGGTGCC
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                                                                                                                                                                                                         A Status: preliminary; translation not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-130 < KLLE>
A; Cross-references: EMBL:X72478; NID:g441424; PIDN:CAA51146.1; PID:g441425
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 33-107/Domain: immunoglobulin homology < INM>
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C)Accession: C21056
R;Bentley, D.L.; Rabbitts, T.H.
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R;Bentley, D.L.; Rabbitts, T.H.
R;Bentley, D.L.; Rabbitts, T.H.
A;Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicat A;Reference number: A21056; MUID:83129397; PMID:6402305
A;Accession: C21056
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A;Accession: 135 CGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAGCC 195 CCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGC 255 GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTT 315 GCAACTTATTACTGCCAACAGTATGATAGTTACCCGTACACTTTTTGGCCAGGGGACCAAG 375 AGATGTGACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGGAGACAGA 120 21 LeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThrCys 40 9 80 9 20 20 C;Species: Homo sapiens (man) C;Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000 1 ProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuProGlyAlaArgCysAlaIleGln MetAspMetArgValLeuAlaGlnLeuLeuGlyLeuLeuLeuLeuCysPheProGlyAla 76 ATGACCCAGTCTCCATCTCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGT ATGGACATGGAGTTCCCCGTTCAGCTCCTGGGGCTCCTGCTGCTTCCCAGGTGCC CCCGTTCAGCTCCTGGGCCTCCTGCTCTGTTTCCCAGGTGCCAGATGTGACATCCAG A;Cross-references: GB:J00248; NID:g185991; PIDN:AAA59094.1; PID:g185992 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;38-112/Domain: immunoglobulin homology <IMM> Ig kappa chain precursor V region (HK137) - human (fragment) 109 10 0 0 1117 1107 55 50 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Matches: Conservative: Mismatches: Indels: Gaps: Gaps: US-08-728-463B-208 (1-439) x C21056 (1-117) (1-125)US-08-728-463B-208 (1-439) x S40349 CTGGAGATCAAACGA 390 2.68e-42 555.00 95.73% 91.45% 557.00 92.00% 87.20% 70.42% Percent Similarity: Best Local Similarity: Query Match: DB: Percent Similarity: Best Local Similarity: Alignment Scores: 376 н 136 41 196 256 81 316 101 121 21 19 61 Query Match: Pred. No.: C21056 ò 엄 ò g ò q ò 엄 8 셤 ò g ò 요 ò g ò g

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19 Kappa chain V-J-C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C;Accession: 840352 3.348-3271, 1993 R;Klein, R: Jaenichen, R.; Zachau, H.G. Eur. J. Immunol. 23, 3348-3271, 1993 A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: 840312; MulD:94080891; PMID:8258341 A;Reference number: 840312; MulD:94080891; PMID:8258341 A;Redecule type: mRNA A;Resession: 840352 A;Retuus: preliminary; translation not shown A;Residus: 1-131 «KLES A;Rese references: EMBL:XZ2462; NID:9441392; PIDN:CAA51130.1; PID:9441393 C;Superfamily: immunoglobulin V region; immunoglobulin homology ciMM>
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C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C;Accession: S40357
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Accession: S40312; MUID:94080891; PMID:8258341
A;Accession: S40357
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A;Coccession: Accession: Accession and their hypermutation.
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A; Residues: 1-127 <KLE>
A; Cross-references: EMBL:X72477
C; Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                            AAACCAGAGAAAAGCCCCTAAAGTCCCTGATTCTGCATCCAGTTTGCAAAGTGGGGTC
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'Species: Homo sapiens (man)

'Bate: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

'Accession: 540353

'Klein, R.; Jaenichen, R.; Zachau, H.G.

'Title: Expressed human immunoglobulin chi genes and their hypermutation.

'Reference number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                     CCTAAGTCCCTCATCTATTCTGCATTCTGCAAAAGTGGGGTCCCATCAAGGTTCAGC
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-104/Domain: immunoglobulin homology <IMM>
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C;Keywords: heterotetramer; immunoglobulin F;33-107/Domain: immunoglobulin homology <IMM>
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bentley D.L., Rabbitts T.H.;
"Human immunoglobulin variable region genes -- DNA sequences of two V
kappa genes and a pseudogene.";
Nature 288:730-733(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=83129397; PubMed=6402305;
Bentley D.L., Rabbitts T.H.;
"Evolution of immunoglobulin V genes: evidence indicating that
recently duplicated human V kappa sequences have diverged by gene
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Copyright (c) 1993 - 2003 Compugen Ltd.
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"Immunoglobulin genes of the kappa light chain type from two human
lymphoid cell lines are closely related.";
Nucletc Acids Res. 12:6995-7006(1984).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-1.
                                                                              FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-I region Walker precursor.
Homo sapiens (Human)
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use by non-profit institutions as long as its content is in no way entities and this statement is not removed. Usage by and for commercial or send an emili to license agreement (See http://www.isb-sib.ch/announce/or send an emili to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                IG KAPPA CHAIN V-I REGION WALK FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                    FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region HK102 precursor (Fragment).
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Matches:
Conservative:
Mismatches:
Indels:
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127 ATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCA 186
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-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
                                                                                                                                                                                                                                         Homo Sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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FRAMEWORK-4.
BY SIMILARITY.
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HSCP; PO1607; IREI.
INTERPRO; IPR003006; Ig_MHC.
InterPro; IPR003566; Ig_V.
R Pfam; PF00047; ig; 1.
R SWART; SWO0406; IGV; 1.
R Immunoglobulin V region; Bence-Jones protein.
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Matches:
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region Kue.
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                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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FRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEMORK-2.
COMPLEMENTARITY-DETERMINING-2.
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Matches:
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Bentley D.L., Rabbitts T.H.;
"Human immunoglobulin variable region genes kappa genes and a pseudogene.";
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InterPro; IPR003596; IG_V.
Ffam; PP00047; ig; 1.
FMART; SM00406; IGv.
Immunoglobulin V region; Signal.
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Best Local Similarity:
                                                                 NCBI_TaxID=9606;
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X MEDLINE=6174817; PubMed=3083240;

RA Daulet F.E., O'Connor T.P., Benson M.D.;

RI "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";

RL MO1. Immunol. 23:73-78 (1986).

DR PIR; A01878; K1HUBN.

HSSP; P80362; 1WTC.

DR InterPro; IPR003066; Ig MHC.

DR InterPro; IPR003066; Ig MHC.

DR Ffan; P80047; ig;.1.

DR SMART; SM00406; IGv; 1.

KW Immunoglobulin V region; Amyloid.

FRAMEWORK-1.

TOWN: EMERITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           247 AGGITCAGCGGCAGIGGAICTGGGACAGAITTCACTCTCACGATCAGCAGCCTGCAGCCT
                                                          13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-AUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region BAN
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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Matches:
Conservative:
Mismatches:
Indels:
                                               108 AA
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101 GlyThrLysLeuAspileLysArg 108
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487.00
94.44%
84.26%
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Best Local Similarity:
Query Match:
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KVIV_HUMAN
ID FVIV HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                              human
                                             13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
19 kappa chain V-1 région Daudi precursor.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=85514148; PubMed=6091049;
Rlobeck H.G., Combriate G., Zachau H.G.;
"Immunoglobulin genes of the kappa light chain type from two lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG KAPPA CHAIN V-I REGION DAUDI.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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Indels:
  129 AA
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  PRT;
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PIR; A01884; K1HUDI.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
                                        13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last seg
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129 AA;
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us-08-728-463b-208.rsp

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AGGITCAGCGGCAGIGGAICTGGGACAGAITICACTCICACCAICAGCAGCCIGCAGCCI 306
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    GAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGTACACTTTTGGCCAG
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-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
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HSSP; P80162; IMTL.
INTERPO; IPR0013066; Ig_WHC.
INTERPO; IPR0013066; Ig_V.
Pfam; PF00047; ig; 1.
Immunoglobulin V region; Glycoprotein.
CARBOHYD 28 28 N-LINKED (GL
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21-JUL-1986 (Rel. 01, Last sec
15-JUL-1999 (Rel. 38, Last and
15 kappa chain V-I region CAR.
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-!- MISCELLANGOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH WALDENSTROM'S MACROGLOBULINEMIA.
                                        CCATCAAGGTTCAGCGGCAGTGGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
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61 LysProGlyLysAlaProThrLeuLeuIleTyrAlaValSerAsnLeuGlnValGlyVal
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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BY SIMILARITY.
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21-JUJ-1986 (Rel. 01, Last sequence update)
15-JUJ-1999 (Rel. 38, Last annotation update)
15 Appa chain V-I region WEA.
Homo sapiens (Human)
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HSSP; P80362; 1WTL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
Imminoglobulin V region; Monoclonal an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE.
MEDLINE=83273707; PubMed=6410398;
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307 GAAGATTITGCAACTIATTACTGCCAACAGTATGATAGTTACCCGTACACTTTTGGCCAG 366
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                 247 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                      127 ATCACTTGTGGGGGGGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCA
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-I region Hau.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal kappa-type immunoglobulin I chain of subgroup I (Bence-Jones Protein Hau): subdivision within
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                                                                                                                                                              GGGACCAAGCTGGAGATCAAACGA 390
                                                                                                                                                                                 MEDLINE=71032830; PubMed=4097974;
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465.00
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                                61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu***Pro 80
                                                                                                                                                                                                                                                                                                                                                                                                                          A BEDLINE=75659122; PubMed=4215718;
A Laure C.J., Watanabe S., Hilschmann N.;
The primary Structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.). I. The amino acid sequence of the L-chain of
Kappa-type, subgroup I.";
LHOPPE-SELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
HISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
MACROGLOBULIN.
PIR; A01667; KIHUGL.
RSSP, P01607; 1REI.
R HSSP; P01607; 1REI.
R HSSP; P01607; 1g, 1.
R HSSP; P01607; 1g, 1.
R FAMART; SM00406; IG, 1.
R SMART; SM00406; IG, 1.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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COMPLEMENTARITY-DETERMINING-1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-I region GAL.
Homo sapiens (Human).
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                                                                GAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGTACACTTTTGGCCAG 366
                61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
247 AGGTICAGCGCAGIGGAICTGGGACAGAITTCACTCTCACCAICAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                          Altenburger W., Steinmetz M., Zachau H.G.; "Functional and non-functional joining in immunoglobulin light chain
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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PRAMENORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMENORK-2.
COMPLEMENTARITY-DETERMINING-2.
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Matches:
Conservative:
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Indels:
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
RAppa chain V-V region T1 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                     128 AA.
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                                                                                                     GGGACCAAGCTGGAGATCAAACGA 390
                                                                                                                    101 GlyThrArgValGluIleLysArg 108
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MEDLINE=81052342; PubMed=6776411;
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Nature 287:603-607(1980).
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                                                          21 AspileLysMetThrGlnSerProSerSerMetTyrAlaSerLeuGlyGluArgValThr 40
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"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds."
Biochemistry 9:3188-3196(1970).
-i- MISCELLANEOUS: THE C FEGION OF THIS CHAIN HAS THE INV (3) MARKER.
-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=71064023; PubMed=5489770;
Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VI. Amino
acid sequence of the light chain.";
Biochemistry 9:3155-3161(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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FRAMEWORK-3.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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Immunoglobulin
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Biophys. Struct. Mech. 1.139-146(1975).

INSCELLANBOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECTUAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF THE KAAPA CHAIN REI.

INSCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

INSCELLANBOUS: THIS IS A BENCE-JONES PROTEIN.

HSSPP. PO1607; IREI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=72189444; PubMed=5028201;
Schiechl H., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
protein Au).;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman B.E. Schwager P., Sreigemann W., Schramm H.J.;
"The structure determination of the variable portion of the
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              Length:
Matches:
Conservative:
Mismatches:
Indels:
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-Mexppa chain V-I region AU.
Homo sapiens (Human).
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Pred. No.:
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"The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Ones protein Rei); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NOBI_TaxID=9606,
             FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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MEDLINE-76039968; PubMed=1182131;
Bpp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
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Bence-Jones protein.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Rei.
Homo sapiens (Human).
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Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
"Preparative separation of the tryptic hydrolysate of a protein
high-pressure liquid chromatography. The primary structure of a
monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAMEMORR-1.

COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-I region Wes.
Homo sapiens (Human).
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FRAMEWORK-1.
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 367 GGGACCAAGCTGGAGATCAAACGA 390
               101 GlyThrLysLeuGlnIleThrArg 108
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HSSP, P80362; 1WTL.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Bence
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15-JUL-1999 (
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"The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution."; Biochemistry 14:4943-4952(1975).
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                                      -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                      FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                        PIR; A01873; KIHURE.
PDB; 1REI; 17-FEB-84.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
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81 GluAspPheAlaThrTyrPheCysGlnGlnAlaHisSerValProLeuThrPheGlyGly 100

367 GGGACCAACTGGAGATCAAACGA 390 ||||||| ::::::|||||||| 101 GlyThrThrValAspIleLysArg 108

g ò g

Search completed: June 3, 2003, 09:04:07 Job time: 10.327 secs

us-08-728-463b-208.rspt

Run on:

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Q9ul77 homo sapien
Q9ul77 homo sapien
Q9ul77 homo sapien
Q91425 mus musculu
Q95p£6 homo sapien
Q95p£6 homo sapien
Q95p£6 homo sapien
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Q91005 oryctolagus
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Q9np29 homo e
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Q91wf8 mus r
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Q8wuk4 homo
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027418; AAH27418.1; -.
Hypothetical protein:
SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEABI CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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(without alignments)
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                                                                                                                                                                            Description
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                 protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0 , Fgapext
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.8 kDa protein (Fragment).
Busculus (Mouse)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Rodentia; Sciurognathi, Muridae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Mus
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Strausherg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013496; AMH1396.1; -.
InterPro; IPR003006; Ig_MHC.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
NOW_TER 1 1 SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;
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O1-WAR-2002 (TEMBLrel. 20, Created)

O1-MAR-2002 (TEMBLrel. 20, Last sequence update)

O1-JUN-2002 (TEMBLrel. 21, Last annotation update)

Hypothetical 25.7 kba protein.

Hypothetical 25.7 kba protein.

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinalia; Euteleostomi;
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L Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
R InterPro; IPR003599; 19—1.
R InterPro; IPR003599; 19—1.
R InterPro; IPR003599; 19—1.
R InterPro; IPR003599; 19—1.
R InterPro; IPR003599; 19—1.
R InterPro; IPR003596; 19—1.
R SMART; SM00409; 169; 2.
R SMART; SM00409; 169; 1.
R SMART; SM00409; 169; 1.
R SMART; SM00409; 169; 1.
R SMART; SM00409; 169; 1.
R R PR0SITE; PS00290; 16—1.
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SEQUENCE 234 Aa; 25702 MW; 102551C58AC2FA9F CRC64;
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                                                                         322 TATTACTGCCAACAGTATGATAGTTACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAG 381
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      LeuLeulleTyrTyrThrSerArgLeuTyrLeuGlyValProSerArgPheSerGlySer
                                                   GGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACT
                                                                                                                                                                                                                     382 ATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGAA 435
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                             S.M.
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Q9UL70;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
WLX. Liu B., Van der Merwe P.L., Kalis N.N., Berney
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B7BEDC3E41FCCA37 CRC64
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Matches:
Conservative:
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Indels:
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Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035044; AAD56280.1;
HSSP; PO1607; IREI.
InterPro; IPR003066; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGV; 1.
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492.00
94.44%
88.89%
62.20%
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Best Local Similarity:
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                                                                157 AGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAGCCCCTAAGTCCCTGATCTATTCT 216
                                                                                                                                                                                                                                                            277 ITCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGCCAACAG 336
                                                                                                                                                                                                                                                                                                                    337 TATGATAGTTACCCGTACACTTTTGGCCAGGGACCAAGCTGGAGATCAAACGAACTGTG 396
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                                                                                                                                                  17 GCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGCAGTGGATCTGGGACAGAT 276
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051WF8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.9 kDa protein.
Hypothetical 25.9 kDa protein.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae;
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TISSUE-COLON;
Straudborg R.;
Submitted (CTT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015292; AAH15292.1; -.
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR001865; Ribosomal_S2.
PROSITE; PS00290; IG MHC; UNKNOWN_1.
PROSITE; PS00290; IG MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 234 AA; 25929 MW; BODOBOBGEB7812D2 CRC64;
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98
16
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Matches:
Conservative:
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Indels:
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506.00
82.61%
71.01%
63.97%
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Best Local Similarity:
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Pred. No.:
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67 GACATCCAGATGACCCAGTCTCCATCTGTCTGCATCTGTAGGAGACAGAGTCACC 126
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                           MEDLINE=98277139; Pubmed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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Matches:
Conservative:
Mismatches:
Indels:
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EMBL; AF035035; AAD56271.1;
HSSP; P01607; IREI.
InterPro; IPR03006; Ig_MHC.
InterPro; IPR00356f; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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                                               Created)
                  PRT;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
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90.74%
84.26%
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                                                                                                                      Homo sapiens (Human)
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Best Local Similarity:
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01-DEC-2001
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GluAspValAlaThrTyrTyrCysGlnLysTyrAsnSerAlaProArgThrPheGlyPro 100
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                                                                                                                                                                                                                                          Eukaryoča, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                              Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

BEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
U-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 AA; 11738 MW; C06681716C4D16F3 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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EMBL; AF035037; AAD56273.1; -
HSSP; PO1607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003566; Ig_v.
Pfam; PF00047; ig; 1.
SMRT; SM00406; IGv; 1.
                                                                                                                            108 AA
                               GGGACCAAGCTGGAGATCAAACGA 390
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                                                                                                                         PRT;
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91.67%
87.04%
59.80%
                                                                                                                         PRELIMINARY;
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Best Local Similarity:
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DB:
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RESULT Q9UL79

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SEQUENCE FROM N.A.
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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (MaD 7, its light and heavy chains) and construction of a single chain antibody (scfV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF152371; AAD40242.1; -.
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer
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01-MAY.2000 (TrEmBLrel. 13, Last sequence update)
01-MAY.2000 (TrEmBLrel. 13), Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Kappa light chain of Mab7 (Fragment).
Man musculus (Mouse).
Eukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                           MEDIINE=98375893; PubMed=9712075; Adderson E.B., Shikhman A.R., Ward K.E., Cunningham M.W.; Adderson E.B., Shikhman A.R., Ward K.E., Cunningham M.W.; molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes."; J. Immunol. 161:2020-2031(1998).
                                                                                                                                                                                                   11520 MW; 4BB43E9C5B577F16 CRC64;
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96
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                      Interpro; AAB68785.1; -.
Pfam; PF00047; ig; 1.
NON TER 107 107
                                                                                                                                                                                                                                       5.75e-44
463.50
90.83%
88.07%
58.60%
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                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                        NCBI_TaxID=9606;
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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86
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
Kappa 1 light chain variable region (Fragment).
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Conservative:
Mismatches:
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InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 2.
SWART; SW00406; IGV; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
NON TER 1 1 1
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                                                                                                                                                                                       214 AA; 23922 MW;
                                                                                                                                                                                                                                                  2.11e-43
459.00
84.55%
69.92%
58.03%
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EMBL; AF361758; AAK51465.1;
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
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us-08-728-463b-208.rspt

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127 ATCACTIGICGGGGGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCA 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Hypothetical 26.2 kDa protein.
Hypothetical 26.2 kDa protein.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (FBB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC0223452, AAH22362.1; -. Hypothetical protein. SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03B71D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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                         US-08-728-463B-208 (1-439) x Q925S9 (1-127)
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444.50
73.65%
57.43%
56.19%
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TISSUE=LUNG;
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Best Local Similarity:
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Q8TCD0
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MEDLINE=93306687; PubMed=10380019;
MEDLINE=93306687; PubMed=10380019;
Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
Foon K.A., Chatterjee S.K.;
"Construction and characterization of a chimeric fusion protein
consisting of an anti-idiotype antibody minicking a breast cancer-
Hybridoma 18:193-202(1999).
BMBL; AF124721; AAK55120.1;
InterPro. PRO0366; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                              E796FC2217BFCF57 CRC64;
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888
111
228
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Immunoglobulin light chain (Fragment).
                                                                  Length:
Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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               116
12735 MW;
                                                                 9.11e-43
453.00
85.34%
75.00%
57.27%
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445.00
77.95%
69.29%
56.26%
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116 1
116 AA;
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NON_TER 127 1
                                                                                    Percent Similarity:
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Best Local Similarity:
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Q925S9;
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AGGITCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 306
                                                              GAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTAC---CCGTACACTTTTGGC 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 ATCACTTGTCGGGCGAGTCAGGGTATT-------AGCAGCTGGTTAGCCTGG 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerGlyLeuGlnAla 80
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| MetLysLeuProValArgLeuLeu---ValLeuMetPheTrpIleProAlaSerSerSer 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 ATGGAGTTCCCCGTTCAGCTCCTGGGGCTCCTGCTGCTGTTTCCCAGGTGCCAGATGT 66
                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 26.3 kDa protein.
Hypothetical 6.3 kDa protein.
Bus musculus (Mouse).
Bukaryota, Metacoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                               A Strausberg R.;

Lubmitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

B Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC002035; AAH02035.1; -.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003500; Ig_like.

R InterPro; IPR003500; Ig_like.

DR InterPro; IPR003596; Ig_v.

DR SWART; SW00409; IG; 2.

DR SWART; SW00409; IG; 2.

DR SWART; SW00409; IG; 1.

DR SWART; SW00409; IG 11; 1.

DR SWART; SW00409; IG 11; 1.

DR SWART; SW00409; IG 11; 1.

DR SWART; SW00409; IG 11; 1.

DR SWART; SW00409; IG 11; 1.

RW HYPOCHETICAL DIACOLUM.

SQ SEQUENCE 238 AA; 26344 MW; FB2EB06A0BB01330A CRC64;
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                                                                                                                                 364 CAGGGGACCAAGCTGGAGATCAAACGA 390
                                                                                                                                                    ProGlyThrLysValAspIleArgArg 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-728-463B-208 (1-439) x Q99M37 (1-238)
                                                                                                                                                                                                                                  PRT;
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411.00
70.27%
56.08%
51.96%
                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
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Best Local Similarity:
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247
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                                                                                                                                                                                               292 AGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCG 351
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101 ThrargValGluAlaGluAspValGlyValTyrPheCysMetGlnGlyThrHisTrpPro 120
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               1 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
172 TATCAGCAGAAACCAGAAAAGCCCCTTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C., "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                 Q9UL81;
Q9UL81;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 19, Last senotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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90
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Matches:
Conservative:
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Gaps:
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EMBL; AF035033; AAD56269.1; -.
HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                     107 AA
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                                                                                                                                                                                                                                                              TTCATCTTCCCGCCATCTGATGAA 435
                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=98277139; Pubmed=9614934;
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88.078
82.578
55.448
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Query Match:
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Pred. No.:
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Q9UL81
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292 AGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCG 351
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100 SerArgValGluAlaGluAspLeuGlyValTyrTyrCysPheGlnGlySerHisValPro 119
                                                                                           SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACATCCAGATGACCCAGTCTCCATCTCTGTCTGCATCTGTAGGAGACAGAGTCACC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 AGGITCAGGGGGGGGGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGGAGCCT 306
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STRAIN=C3H/HEJ-LPR/LPR;
MEDLINE=56409289; PubMed=8814271;
MEDLINE=56409289; PubMed=8814271;
MIOCH M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
"Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
Eur. J. Immunol. 26:2225-2233(1996).
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68506D75613DBFBE CRC64;
                                                                                                                                                                                                                                                                      09VIJO;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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108 AA; 11859 MW;
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rPro; IPR003599; IG:
rPro; IPR003006; IG MHC.
rPro; IPR003596; IG-V.
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405.00
85.19%
70.37%
51.20%
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MART; SM00409; IG; i.
MART; SM00406; IGv;
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Title: Perfect score:

Sequence:

Scoring table:

Total number of

Searched:

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antiallergic, antiuleer; neuroprotective; antithyroid; vacorropic; immunosuppressive; dermatological; antiinflammatory; hepatotropic; activation inducible lymphocyte immunomodulatory molecule; AILIM; monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergy; contacttype dermatitis; chronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammatois; graft versus host reaction; immune rejection; intestinal immunity;
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SUMMARIES
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AAY96289
AAR38162
AAR20058
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                                                                                                                                    12-MAR-2002 (first entry)
                                                                              Length
                                                     Query
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                                               Result
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-DB=A_Geneseq_101002_QFWT=fastan -SUFFTX=rsq -MINMATCH=0.1_LOOPEX.e
-UCOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blooum62 -TRANS=hun40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_NAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pto -NOFM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USR=US08728463_GCN_1_1353_grunat_0362003_085613_16797 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORE=0 -WAIT -DSPELOCK=100 -LONGLOG
-FRAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDST=7
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                                                                                                                              protein search, using frame_plus_n2p model
                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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Human vkappa65.15
Human DNA vkappa65
Amino acid sequenc
TR8-SG9 CDR grafte
Human IGFAM-12 imm
JP11127855 Seq ID

Immunoglobulin kap Human novel protei Amino acid sequenc

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Immunoglobulin kap

CD4-specific CDR-g Thrombopoietin ago The kappa chain of 93KA9 anti-Varicel

Database

Human novel protei Human anti-tumour TRO005 HuMab kappa

Human protein sequ

Human ovarian anti TRO005 Humab kappa TRO005 Humab kappa Human IGFAM-5 immu Human anti-RSV mon Humansed 5G1.1 VL

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IgG antibody 2.6.1

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Human anti-HBs lig

Human immune syste

Anti-human AILIM m

Human IGFAM-10 imm

Human protein SEQ Human IGFAM-1 imm

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81 ProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
                                                                                                                                                                                         41 ValThrileThrCysArgAlaSerGlnGlylleSerArgLeuLeuAlaTrpTyrGlnGln 60
                                                                   CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
                                             181 AAACCAGAGAAAGCCCCTAAGTCCCTGATCTATTCTGCATTTGCAAAGTGGGGTC
                                                                                                                                                                      CAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGTACACTTTT
                                                                                                                                                                                                                                 GOCCAGGGGACCAAGCTGAAACGAACTGTGCCTGCACCATCTGTCTTCATCTTC
                                                                                                                                                                                                                                                   Immune response protein; HIRP1; human; immunological disease; cell_prollferation; cancer; anti-HVV; antiallergic; antianaemic; antiasthamatic); antiarreriosclerotic; antipsoriatic; immunosuppressive; dermacological; antidiabetic; antinflammatory; antiulcer; virucide; antiacetric; antiarrhritic; antiulcer; virucide; antiacetril; fungicide; protozoacide; anthalmintic; vulnerary; hepatotropic; cytostatic; therapy; diagnosis; vaccine; immunoglobulin.
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/note= "T-cell glycoprotein CD8 motif"
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/note= "immunoglobulin domain motif"
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/label= Mature protein
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                        원
                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel human antibody (I), preferably a human conclonal antibody which binds to an activation inducible lymphocyte monoclonal antibody which binds to an activation inducible lymphocyte commondulatory molecule (AILIM). (I) is useful for modulating soft proliferation transduction into a cell mediated by AILIM, for modulating proliferation of a transduction into a cell mediated by AILIM, commondulating proliferation of a Cytokine from against AILIM-expressing cells, and for inducing antibody-dependent cytocxcity AILIM-expressing cells and/or immune cytolysis or apptobls of prophylaxis of delayed type allergy. (I) is useful for treating, preventing and continulatory transduction, and for inhibiting the onset and/or prevention and/or treatment of the diseases associated with AILIM-mediated costimulatory transduction, and for inhibiting the onset and/or prevention and/or treatment of the useful for suppression.

Costimulatory transduction, and for inhibiting the onset and/or prevention and/or treatment of the useful for suppression.

Costimulatory transduction, and for inhibiting the onset and/or prevention and/or treatment of the useful for suppression.

Control inflammatory dermacosis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic disease, immune rejection, disorders such as immunity, specifically inflammatory intestinal disorders such as immunity, specifically inflammatory intestinal disorders such as immunity, specifically inflammatory intestinal disorders such as immunity, particulation antiques no serious immunorable antique to antigenicity contact to human, i.e., human anti-mouse antigenicity (HaMA) in a host.

Cacid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATGTGACATCCAGATGACCCAGTCTCCTCACTGTCTGCATGTGTAGGAGACAGA 120
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                                                                                                                                                                                                                                                                                                          New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGACATGGAGTTCCCCGTTCAGCTCCTGGGGGCTCCTGCTGTTGCTAGTGCTCC
 ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                    Claim 30; Page 270-271; 300pp; English.
                                                                                                                        15-MAY-2001; 2001WO-JP04035.
                                                                                                                                                      18-MAY-2000; 2000JP-0147116.
30-MAR-2001; 2001JP-0099508.
                                                                                                                                                                                                    (NISB ) JAPAN TOBACCO INC.
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                                                                                                                                                                                                                                                              WPI; 2002-075313/10.
N-PSDB; AAS99473.
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                                                             WO200187981-A2.
                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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The invention is based on the discovery of new human immune response proteins (HIRP), the polynucleotides encoding them, and the use of these compositions for the diagnosis, treatment or prevention of immunological and cell proliferative disorders.

The present sequence is that of human immune response protein 1 (HIRP), incyte ID No. 6100311CDI), as determined from a polynucleotide assembled e.g. from a lung adenocarcinoma cDNA library clone. The amino acid sequence shows homology, from a polynucleotides suggest that it may be an immunoglobulin. HIRP polynucleotides and polypeptides are useful for the diagnosis, creatment and prevention of cell proliferative disorders (e.g. cancers, arteriosclerosis, actinic keratosis, burstits, mixed connective tissue disease (MCTD), myelofibrosis, psoriasis, leukaemia, hepstitis, cirrhosis and atherosclerosis), and immunological disorders e.g. AIDS, Addison's disease, adult respiratory distress syndrome (ARDS), anaemia, asthma, autoimmune crown sisces actorphic gastritis, Goodpasture's syndrome, crown sisces, context dermatitis, diabetes mallitus, cholecystitis, crown tiple sclerosis, irritable bowel syndrome, osteoporosis, multiple sclerosis, irritable bowel syndrome, osteoporosis, hatterioris, diabetes mallitus, cholecystitis, crown tiple fungal, parasitic, protozoal and helminthic infections. The polypeptides are also used to screen for agonist and antagonist and atherapeutic use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human immune response proteins, for treating immunological disorders and cell proliferative disorders, and for assessing the effects of exogenous compounds on the expression of HIRP molecules
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/note= "immunoglobulin domain motif"
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/note= "Ig.MHC motif"
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1 ATGGACATGGAGTTCCCCCGTTCAGCTCCTGGGGCTCCTGCTGCTGTTTCCCAGGTGCC

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165
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Immunoglobulin superfamily proteins, the agonist and antagonist of the
                                                                                                                                                                                                         61 AlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeulleTyrLysAlaSerSer
                                                                                                                                                                     GCCTGGTATCAGCAGAAACCAGAGAAAGCCCCTAAGTCCCTGATCTATTCTGCATCCAGT
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                                                                        GTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGC-------AGCTGGTTA
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Yang J;
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/label= signal_peptide
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/label= Ig_domain
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/label= IGFAM-9
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98US-0113635.
99US-0128194.
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Lal P, Hillman JL,
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N-PSDB; AAA27389.
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07-APR-1999;
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protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders
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Claim 1; Page 85; 105pp; English.

The present sequence is the human immunoglobulin superfamily protein IGFAM-9. Its gene was isolated from a cDNA library of breast tumour tissue. It is expressed in reproductive, gastrointestinal and immune and haematopoletic tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for diagnosing and treating many diseases, including cancer, immune system arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus, emphysema, Graves disease, hepatitis, comultiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative colitis, compilcations of systemic lupus erythematosus and ulcerative colitis, compilcations of cancer, haemodialysis and extracorporeal circulation, trauma and chematopoietic cancer (such as leukaemia) and infections caused by compilcation, trauma and contexts.

236 AA; Sequence

236 126 7 7 0 Length: Matches: Conservative: Mismatches: Indels: 651.00 91.72% 86.90% 82.30% Similarity: Percent Similarity: Best Local Similarit; Query Match: DB: Alignment Scores: Pred. No.:

US-08-728-463B-208 (1-439) x AAY96297 (1-236)

AGATGTGACATCCAGATGACCCAGTCTCCATCCTCACTGTGCATCTGTAGGAGACAGA 120 121 GTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAG 180 360 240 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 300 420 20 40 9 80 ATGGACATGGAGTTCCCCGTTCAGCTCCTGGGGGTCCTGCTGCTGTTTTCCCAGGTGCC 181 AAACCAGAGAAAGCCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTC ||||||| LysProGlyThrAlaProLysSerLeulleTyrAspThrSerSerLeuGlnSerGlyval CAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGGTACACTTTT 361 GGCCAGGGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTC CCGCCATCTGATGAA 435 61 61 241 121 301 421 ò 셤 ò 셤 g ò ò B. ò 셤 ઠે 요 ò 요 ò

RESULT 4 ABP41164

ABP41164 standard; Protein; 260 AA.

ABP41164;

23-AUG-2002 (first entry) XXXXXX

Human ovarian antigen HRACW30, SEQ ID NO:2296.

Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoes, endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; acatiovasecular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosom mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antinflammatory; gynaecological; reproductive; chromosome 2p12.

Homo sapiens.

WO200200677-A1.

03-JAN-2002.

07-JUN-2001; 2001WO-US18569

(HUMA-) HUMAN GENOME SCI INC

07-JUN-2000; 2000US-209467P.

Rosen CA;

Birse CE,

2002-147878/19.

N-PSDB; ABQ54241.

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases

Claim 11; SEQ ID No 2296; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABD64131-ABD56305), and also concompasses polypeptides 104 identical and polynucleotides 954 identical to the sequences of the invention. The invention additionally relates to combinant vectors and host calls comprising human ovarian antigen of covarian antigen polynucleotides and polypeptides in diagnoshing, convarian antigen polynucleotides and polypeptides in diagnoshing, treating, prognosing or preventing various ovary and/or breast cancer, and disorders. Suck conditions include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, copyloypetic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine shock syndrome), inflammatory conditions (e.g., maetitis, only multo disorders (e.g., chlamydia, HIV, toxoplasmosis, and toxic cyaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune ophoritis, spetemic lupus erythematosus), crepticatory disorders, neurological disorders, gastrointestinal disorders (e.g., anaemia), cardiovascular disorders only multipary system disorders (e.g., anaemia), cardiovascular disorders only multipare ovarian antigen polypeptides may compuned the compounds which curcher be used for gene therapy, chromosome mapping, in the conductor of individuals and in forensic analysis, and the cused in disease diagnosis, drug targeting and phenocyphing. The present cuseful in disease diagnosis, drug targeting and phenocyphing. The printed sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed compount of the printed compount of the printed of the printed compount of the printed compount of the printed compount of the printed of the printed compounts a human ovarian antigen of the printed compounts a human ovarian antigen of the printed compounts a human ovarian antigen of the printed compounts and the compounts and the compoun ftp.wipo.int/pub/published_pct_sequences.

Sequence

3.46e-58 638.00 89.66% Percent Similarity: Alignment Scores: Pred. No.:

260 125 5 Length: Matches: Conservative:

80

300

360

420

us-08-728-463b-208.rag

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Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders
                            CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
                                                                                                                                                                       GGCCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTC
              AAACCAGAGAAAAGCCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGGTC
                                                                                                                   CAGCCTGAAGATTTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGTACACTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                         Human; immunoglobulin; IGFAM-1; IGFAM; immune disorder;
infection; inflammation; haematopoiesis; AIDS; allergy.
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Yang J;
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/label= signal_peptide
23..237
/label= IGFAM-1
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/label= Ig_domain
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/label= Ig_domain
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98US-0113635.
99US-0128194.
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Lal P, Hillman JL,
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22-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel human monoclonal antibodies. The antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II receptor, resulting in the inhibition of the signal transduction of human TGF-beta into cells. The antibodies can be used for the prevention and treatment of diseases associated with the production of TGF-beta, such as tissue fibrosis in the lung, liver, skin, kidney or other tissues, atherosclerosis, atopy, keloid and arthritis. The present sequence was used in the present invention.
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                                                                                                                                                                    Human, antiarthritic; cardiant; monoclonal antibody; keloid; arthritis; Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy; signal transduction inhibition; tissue fibrosis; atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human monoclonal antibodies recognizing human TGR-beta II receptor, useful for treating TGF-beta associated diseases such as tissue fibrosis -
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AAB99115 standard; Protein; 146
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634.00
90.34%
86.21%
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                                                                                                                                              Human protein SEQ ID 12.
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Best Local Similarity:
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                                                                                                                                                                                                                                                 WO200136642-A1
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                                                                                                                   22-AUG-2001
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                                                                                          AAB99115;
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121 GTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAG 180
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LysProGlyLysAlaProLysLeulleTyrAlaAlaSerSerLeuGlnSerGlyval
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418 TTCCCGCCATCTGATGAA 435
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Best Local Similarity:
          07-APR-1999;
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Lu DAM,
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85 LysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSer***LeuGlnSerGlyVal 104
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                                                                                                                      CCATCAAGGTTCAGGGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
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                                                                                                                                                                                                                 cancer;
                                                                                                                                                                                                                                                                                                                                                                              Human; immunoglobulin; IGFAM-10; IGFAM; immune disorder;
infection; inflammation; haematopoiesis; AIDS; allergy.
       500
    Mismatches:
Indels:
                               US-08-728-463B-208 (1-439) x ABP41164 (1-260)
                     Gaps:
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/label= signal_peptide
23..237
/label= IGFAM-10
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/label= Ig_domain
193..236
/label= Ig_domain
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/label= Ig_domain
                                                                                                                                                                                                                                                                                                                  AAY96298 standard; protein; 237
                                                                                                                                                                                                                                                                                                                                                               Human IGFAM-10 immunoglobulin.
                                                                                                                                                                                                                                                                      CCGCCATCTGATGAA 435
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   86.21%
80.66%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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22-DEC-1998;
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          Query Match:
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Peptide
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40

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Length:
Matches:
Conservative:
Mismatches:

3.83e-58 637.50 90.41% 87.67% 80.59%

Gaps:

300

357 120

240

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The present sequence is the human immunoglobulin superfamily protein is IGFAM-10. Its gene was isolated from a cDNA library of colon tissue. It is expressed in reproductive, gastrointestinal and cardiovascular tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for diagnosing and treating many disease, including cancer, immune system atteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's arteriosclerosis, sporiasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative colitis, complications of cancer, haemodialysis and extracorporeal circulation, trauma and haematopoietic cancer (such as leukaemia) and infections caused by
                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders
                                                                                                                                                                 Guegler KJ, Gorgone GA, Baughn MR;
Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 85-86; 105pp; English.
                                                                                                                                                         Tang YT, Corley NC,
Lal P, Hillman JL,
99US-0128194
                                                                    (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                WPI; 2000-387796/33.
N-PSDB; AAA27390.
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B-cell; immunoglobulin g; cancer; tumour.
       88BV59, ATCC CRL 10624.
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                                                                                                                                               Homo sapiens
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                                                                                                                             CG GFAM-1. Its gene was isolated from a cDNA library of synovial membrane tissue. It is expressed in reproductive, gastrointestinal and cardiovascular tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for diagnosing and treating many diseases, including cancer, immune system cd sorders (such as inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma, atherosclerosis, asthma, atherosclerosis, cholecystitis, crohn's comultiple sclerosis, asthma, atherosclerosis, cholecystitis, scleroderma, csystemic lupus erythematosus and ulcerative colitis), complications of cancer, haemodialysis and extracorporeal circulation, trauma and concer, haemotopoietic cancer (such as leukaemia) and infections caused by take become and viruses, fungi or parasites.
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Mismatches:
Indels:
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Matches:
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                                                                Claim 1; Page 77-78; 105pp; English.
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The 88BV59 kappa light chain sequence is indicated by the posns. of the CDRs and the constant region exon. 88BV59 utilises Vx1 and Jx5. The first NH2 terminal 22 residues were confirmed by AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transformed human B-cell line for monoclonal antibody prodn. for cancer diagnosis - prepd from peripheral blood B-cells of cancer patients actively immunised with autologous tumour antigen, for
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Matches:
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                                                           denoted AA#1
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Location/Qualifiers
1..214
/*tag= a
/label= 1st AA denote
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                                                                                       /*tag= b
/label= CDR 1
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/label= CDR
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label= CDR
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N-PSDB; AAQ43773.
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LysProGlyLysValProLysLeuLeulleTyrLysAlaSerSerLeuGluSerGlyVal
                                                    The variable region of the light chain is used in a recombinant protein with the variable region from the heavy chain of 3D6, the two V regions being joined by a linker. The recombinant protein binds to HIV gpl60. See also AAQ20066 and AAQ20068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immunoglobulin; IGFAM-13; IGFAM; immune disorder; cancer;
infection; inflammation; haematopoiesis; AIDS; allergy.
HIV-1 - contains variable region of antibody derived from 3D6 cell line, used for detecting HIV-1 antigen
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122
122
122
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Matches:
Conservative:
Mismatches:
Indels:
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1..22
/label= signal_peptide
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                              Claim 3; Page 28; 52pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human IGFAM-13 immunoglobulin.
                                                                                                                                                       2.32e-57
630.00
90.34%
84.14%
79.65%
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                                                                                                                        234 AA;
                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                            Alignment Scores:
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|ProLygLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPheSer
                                                           GCAACTTATTACTGCCAACAGTATGATAGTTACCCG---TACACTTTTGGCCAGGGGACC
                                                                                                      CCTAAGTCCCTGATTCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGC
                                              GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant protein which binds to complex viral antigen and
                                                                                                                                                                                                                                                                                                                                     Plasmid pUC1D6LC; human immunodeficiency virus; AIDS; complementarity determining region.
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/label= Framework_4
128..234
/label= Constant_region
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/label= CDR_2
79..110
/label= Framework_3
                                                                                                                                                                                                                                                                                                                Light chain of 3D6 anti-HIV antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                        3.45
label= Framework_1
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/label= Framework_2
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/label= signal
23..234
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|abel= CDR_1
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/label= CDR_3
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                                                                                                                                                                                                                                                                                           (first entry)
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N-PSDB; AAQ20067.
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                                                                                                                                                                                 GAA 435
                                                                                                                                                                                                143 Glu 143
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   196
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                                                                                                                                                                                                                                                                                                                                                                                             Key
Peptide
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Region
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TTTGGCCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTTCATC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiarteriosclerotic; antiathmatic; antidiabetic; nephrotropic; cancer; antigout; dermatological; antithyroid; virucide; hepatotropic; antibody; immunosuppressive; cytostatic; fungicide; protrozocide; antibody; gene therapy; diagnostic; immunological disorder; viral infection; bacterial infection; fungal infection; parasitic infection; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a human immune system molecule (IMOL) encoded by the cDNA isolated as clone 1666486 from the Incyte BMARNOT03 library. The human IMOLS (AAB15536-B15550) and their encoding polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AAAST775-AS789), and compositions comprising them are useful for the diagnosis, treatment or prevention of immunological disorders, influence and call proliferative disorders, including cancer. The IMOL may be used to treat or prevent disorders associated with decreased expression or activity of IMOL, such as immunological disorders (e.g. inflammation, actinic keratosis, AIDS, Addison's disease), haematopoietic cancer, infections caused by virus (e.g. adenovirus, parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,
                                                                                                                       CAGCCTGAAGATTTTGCAACTTATTACTGCCAACAG---TATGATAGTTACCCGTACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human immune system molecules 1-15 and polynucleotides encoding them useful for diagnosing, treating or preventing e.g. immunological disorders, infections, cell proliferative disorders, microbial
               CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
 AAACCAGAGAAAGCCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lu DAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system molecule from Incyte clone 1666486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Azimzai Y,
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                                                                                                                                                                                                                                                                                                                                         AAB15546 standard; Protein; 237 AA
                                                                                                                                                                                                                                              TTCCCGCCATCTGATGAA 435
                                                                                                                                                                                                                                                               99US-0127852.
99US-0132647.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE PHARM INC
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 181
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                                                                                                                                                                                                                                                                                                                                                       AGATGTGACATCCAGATGACCCAGTCTCCATCTCACTGTCTGCATCTGTAGGAGACAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metaspmetargval Proalagin Leu Leu Gly Leu Leu Leu Leu Trp Leu Arggiyala
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Matches:
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Yang J;
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                            38..112
/label= Ig_domain
150..219
/label= Ig_domain
                                                                                    US-08-728-463B-208 (1-439) x AAY96301
23..237
/label= IGFAM-13
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98US-0113635.
99US-0128194.
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Lal P, Hillman JL,
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629.50
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84.93%
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Query Match:
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Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g. Plasmodium, Trypanosoma, intestinal protozoa), cell proliferative disorders (e.g. actinic keratosis, arteriosclerosis, bursitis), and cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also useful as immunogens for the development of antibodies that specifically recognizes these peptides. The polymucleotides may be used to detect and quantify gene expression in biopside tissues in which capression of IMOL may be correlated with the disease, as targets in a microarray, to detect differences in gene sequences among normal, carrier and affected individuals, and for screening libraries of compounds in drug screening techniques. Antibodies which specifically bid to IMOL may be used for the diagnosis of disorders characterized by expression of IMOL, or in assays to monitor patients being treated with IMOL or agonists, antagonists, or inhibitors of IMOL.
                                                                                                                                                                                                                                                                                                                                                                                   GICACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAG 180
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Best Local Similarity:
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101 GinProGluAspPheAlaThrTyrTyrCysLeuHisHisAsnAsnTyrProLeuSerPhe 120
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                                                                                                                                                                                                                                                                                 Polynucleotides encoding the L and H chains of human anti-HBs
Ab are given in AAQ49941-Q49944. The Ab can be easily produced
large quantities for therapeutic use.
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                                                                                                                                                                                 Tsuruoka
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                              Disclosure; Fig 4-5; 46pp; Japanese.
            Location/Qualifiers
                           /label= sig_peptide
23..236
/label= mat_protein
                                                                                                                                                                               Matsukura S,
                                                                                                                93WO-JP00396
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623.00
90.34%
81.38%
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                                                                                                                                                                                               WPI; 1993-336913/42.
                                                                                                                                                        (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                             236 AA;
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Best Local Similarity:
Query Match:
DB:
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                                                                                                              30-MAR-1993;
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Antibody; Ab; light; heavy; chain; hepatitis B; HB; surface antigen.

Homo sapiens

Human anti-HBs light chain.

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TRO005 HuMab kappa chain protein sequence 3E9K.
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                                                                                                    The present invention describes a method (M1) for producing a human antibody phage display library (I), comprising: (1) providing a nonhuman transgenic animal (II) whose genome comprises human immunoglobulin genes; (2) isolating nucleic acide encoding human antibody chains (III) from lymphatic cells; and (3) forming a library of display packages whose members comprise a nucleic acide encoding (III) which is displayed from the package. The method is used for producing a human antibody display library, e.g., a Fab phage display library. The display method may be used to screen nucleic acide encoding antibody chains obtained from immunised nonhuman transgenic animals, and from this a population of antibodies may be prepared. Production of a human monoclonal antibodies display library using this method means there is no need to immunise thumans with antigens, and the difficulties faced with immortalising B cells are avoided. AAH39958 to AAH30965 and AAB4994 to AAB75056. represent sequences used in the exemplification of the present invention.
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                                  Producing a human antibody phage display library comprises providing a transgenic animal whose genome comprises human immunoglobulin genes and isolating nucleic acids encoding antibody chains from lymphatic cells -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 ATCACTTGTCGGCCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCA
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                                                                                 Example 37; Page 121-122; 161pp; English
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609.00
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The present invention describes a method (M1) for producing a human antibody phage display library (I), comprising: (1) providing a nonhuman transpanic animal (II) whose genome comprises human immunoglobulin genes; (2) isolating nucleic acids encoding human antibody chains (III) from lymphatic cells; and (3) forming a library of display packages whose members comprise a nucleic acid encoding (III) which is displayed from the package. The method is used fenceding (III) which is displayed from the package. The method is used for producing a human antibody display library, e.g., a Fab phage display library. The display method may be used to screen nucleic acids encoding antibody chains obtained from immunised nonhuman transgenic animals, and from this a population of antibodies may be prepared. Production of a human monoclonal antibodies display library using this method means there is no need to immunise humans with antigens, and the difficulties faced with immortalising B cells are avoided. AMI30958 to AMI30066 and AMB74994 to AMB75056 represent sequences used in the exemplification of the present invention.
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Human, antibody, immunoglobulin, interleukin 8, IL8, immunogen;
human antibody phage diaplay library, immunisation; transgenic animal
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(GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
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99US-0453234.
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01-DEC-1999;
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ovarian antigen; ovary; ovarian; breast; cancer;
                                            Human ovarian antigen HVVCI50, SEQ ID NO:4289.
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                 ABP43157 standard; Protein; 139
141 ProProSerAspGlu 145
                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                07-JUN-2001; 2001WO-US18569
                                                                                                                                          07-JUN-2000; 2000US-209467P.
                                    (first entry)
                                                                                                                                                            Rosen CA;
                                                                                                                                                                     2002-147878/19.
                                                                                                                                                                          N-PSDB; ABQ56234.
                                                                                                               WO200200677-A1
                                                                                                       Homo sapiens,
                                    22-AUG-2002
                                                                                                                        03-JAN-2002
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                          ABP43157;
             ABP43157
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76 Argaccongretrocarcorregrerecarciterangeagacagacconrecarior 135
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAACTIATIACTGCCAACAGTATGATAGTTACCCGTACACTTTTGGCCAGGGACCAAG 375
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43 ArgAla***GlnSerIleSerSerTrp***AlaTrpTyrGlnGlnLy9ProGlyLy9Ala 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 CCCGITCAGCICCTGGGGCTCCTGCTCTTTCCCAGGTGCCAGATGTGACATCCAG
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human antibody phage display library, immunisation, transgenic animal.
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(GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
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                                                                                                                                                                                                                                                                                                                                                                                    ovarian cancer; breast cancer; tumour; reproductive system disorder; pinfertility; pregnancy disorder; anovulation; polycystic ovary syndrome; pCOS; ovarian cyst; dysmenorrhoea, endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; dardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases
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APPLICANT: Faulk, Katsunari

APPLICANT: Hori, No. US20020102658Aluaki

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF

TITLE OF INVENTION: DARRACEUTICAL USE THEREOF

TITLE OF INVENTION: DARRACEUTICAL USE OF THEREOF

TITLE OF INVENTION: UNMBER: US/09/859,053

CURRENT FILING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: UP 2001-19508

PRIOR FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30

LENGTH: 236
Sequence 19, Appl
Sequence 128, App
Sequence 128, App
Sequence 10, Appl
Sequence 2, Appli
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Sequence 150, App
Sequence 36, Appl
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Sequence 6, Appli
Sequence 52, Appli
Sequence 2, Appli
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Sequence 9, Appli
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Sequence 13, Appli
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Sequence 4, Appli
Sequence 4, Appli
Sequence 31, Appl
Sequence 15, Appl
Sequence 17, Appl
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Sequence 26, Appl
Sequence 67, Appl
Sequence 2, Appli
Sequence 97, Appl
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Sequence 7, Appli
Sequence 15, Appl
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Sequence 62,
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Pred. No.:
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-MODEL=frame+ n2P model - DEVexlp
-DG-CgnZ 1/USFTO spool/US08728463/runat 03062003_085618_16959/app_query.fasta_1.3690
-DG-CgnZ 1/USFTO spool/US08728463/runat 03062003_085618_-MONNATCH=0.1
-DG-CGnZ 1/USFTO spool/USGTS-bits -START=1 - ENDE-1 - MATRIX=blosum62
-LOOPCL-0 -LOOPCENT=0 - UNITS-bits -START=1 - ENDE-1 - MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 - DGCALIGN=pto -THR SCORE=ptc -THR MAX=100
-THR MIN=0 - ALIGN=15 - MODE=LOCAL -OUTFWT=ptc - NORM=ext - HEAPGIZE=500 -MINLEN=0
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-LONGLGG - DEV TIMEOUT=120 - WARN TIMEOUT=0 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5
-FGAPOP=6 - FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Sequence 24, Appl
Sequence 69, Appl
Sequence 26, Appl
                                                                                                        3, 2003, 09:04:15 ; Search time 18.6525 Seconds (without alignments) 4764.744 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

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4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

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                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                              OM nucleic - protein search, using frame_plus_n2p model
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US-10-006-593-69
US-09-740-002-26
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Maximum Match 100%.
Listing first 45 summaries
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       US-08-728-463B-208 (1-439) x US-09-740-002-24 (1-234)
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ORGANISM: artificial sequence
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J APPLICANT: BRAMS, PHILLIP
J TITLE OF INVENTION: SPECIFIC TO RSV P-PROTEIN AND METHODS FOR THEIR
J TITLE OF INVENTION: SPECIFIC TO RSV P-PROTEIN AND METHODS FOR THEIR
J TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
J TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
J CURRENT APPLICATION NUMBER: 08/09/740,002
CURRENT APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
J PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATCHING VOICE: 21
SEQ ID NO 24
LENGTH: 234
                                                                                                                                                 61 AGAIGIGACAICCAGAIGACCCAGICTCCAICCICACTGICTGCAICTGIAGGAGACAGA 120
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|MetAspWetArgValProAlaGinLeuLeuGiyLeuLeuLeuLrpPheProGlySer
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Patent No. US20020001798A1
GENERAL INFORMATION:
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Publication No. US20030049683A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Frederickson, Shana
APPLICANT: Remanaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2
CURRENT PLING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR FILING DATE: 2000-12-05
PRIOR PLICATION NUMBER: US 60/251,48
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
SRIOR PRIOR DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 118
SEQ ID NOS: 118
SEQ ID NOS: 128
LENGTH: 236
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                                  41 ValThrIleThrCysArgAlaSerGlnSerIleAlaSerTyrValAsnTrpTyrGlnGln
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Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: FC23013A
CURRENT APLICATION NUMBER: US/10/153,382
CURRENT APPLICATION NUMBER: 60/293042
PRIOR APPLICATION NUMBER: 60/293042
PRIOR PILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VET: 2.1
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Matches:
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567.00
94.31%
90.24%
71.68%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No.:
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Sequence 26, Application US/09740002

Patent No. US2002000198A1

GENERAL INFORMATION:

APPLICANT: BRAMS, PETER

APPLICANT: MORROW, PHILLIP

TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

CURRENT PELLING DATE: 200-12-20

PRIOR PILLING DATE: 999-06-18

PRIOR FILLING DATE: 999-06-18

PRIOR FILLING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 26

LENGTH 234
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585.50
89.04%
80.82%
74.02%
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; ORGANISM: Homo sapiens
US-09-740-002-26
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Best Local Similarity:
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US-09-740-002-26
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127 ATCACTIGICGGGCGAGICAGGGTATTAGCAGCIGGTTAGCCTGGTATCAGCAGAAACCA 186
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                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Weil Charles
APPLICANT: Chapman, Andrew Paul
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0095
CURRENT APPLICATION NUMBER: US/09/949,559
CURRENT APPLICATION NUMBER: 0013810.7GB
PRIOR FILING DATE: 2000-06-06
PRIOR FILING DATE: 2000-06-06
PRIOR FILING DATE: 2001-66-06
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PATENTIN VERSION 3.1
                                                                                Sequence 128, Application US/09949559
Patent No. US20020151682A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Pred. No.:
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LENGTH: 214
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US-09-875-221A-128
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Matches:
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Mismatches:
Indels:
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GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew George
APPLICANT: King, David John
APPLICANT: King, David John
TILE PEFERRNCE: Carp-0089
CURRENT APPLICATION NUMBER: US/09/875,221A
CURRENT APPLICATION NUMBER: GB0013810.7
PRIOR APPLICATION NUMBER: GB0013810.7
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 130
SEQ ID NO 128
LENGTH: 214
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Sequence 128, Application US/09875221A
Publication No. US20030026805A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity:
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Length: Matches: Conservative: Mismatches: Indels: Gaps:

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APPLICANT: Klimowski, Laura C.
APPLICANT: Klimowski, Laura
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: PROGARMYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: P1793R1
CURRENT FILING DATE: 2002-03-26
FRIOR APPLICATION NUMBER: US 60/256,164
PRIOR APPLICATION NUMBER: US 60/256,164
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 10
LENGTH: 237
TYPE: ...
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Matches:
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Mismatches:
Indels:
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APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA W.--
                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: anti-VEGF light chain US-10-020-786-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        418 TTCCCGCCATCTGATGAA 435
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553.00
90.48%
85.71%
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Best Local Similarity:
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US-09-056-160B-100
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Pred. No.:
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GICCCATCAAGGTICAGCGGCAGTGGAICTGGGACAGATTTCACTCTCACCATCAGCAGC 297
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Mismatches:
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
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                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                            28,616
3R: P1093R2
                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-10-011-125-2
, Sequence 2, Application US/10011125
; Patent No. US20020142388A1
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                            NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
South San Francisco
California
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 237 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      550.00
90.48%
84.92%
69.53%
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Best Local Similarity:
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TELEFAX: 6
                                                     94080
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 CITY: SOUSTATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: SITE

† LOCATION: (120)

† OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-800-729-150
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                                                                            Length:
Matches:
Conservative:
Mismatches:
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Fatent No. US20020068319A1
GENERAL INFONATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REPERENCE: PZ044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
FRIOR PRILING DATE: 2000-09-22
FRIOR PELING DATE: 1999-09-24
FRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PATENTIN VET. 2.00
                                                                                                                                                     Gaps:
                                                                         4.17e-41
546.50
82.07%
77.24%
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                  i ORGANISM: Homo sapiens
US-09-800-729-152
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                  Percent Similarity:
Best Local Similarity:
                                                          Alignment Scores:
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Pred. No.:
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21 AlaTyrAlaAspIleGinLeuThrGinSerProSerSerLeuSerAlaSerValGiyAsp 40
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Matches:
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Mismatches:
Indels:
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Patent No. US2002006319A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR PILING DATE: 2000-09-22
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SSOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                  US-08-728-463B-208 (1-439) x US-10-011-125-2 (1-491)
APPLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT APPLICATION NUMBER: US/10/011,125
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
LENGTH: 491
                                                                                                                                                                                         ; OTHER INFORMATION: Sequence is synthesized US-10-011-125-2
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ORGANISM: Artificial Sequence
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Best Local Similarity:
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LENGTH: 235
TYPE: PRT
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                                                                                                                                        ProLysSerLeulleTyrSerAlaSerIleLeuGlnSerGlyValProSerLysPheSer
                                                                                                                                                                              GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTT
                                                                                                                                                                                           GCAACTTATTACTGCCAACAGTATGATAGTTACCCGTACACTTTTGGCCAGGGGACCAAG
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; Publication No. US20030077739A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Laura
; APPLICANT: Simmons, Laura
; APPLICANT: Andersen, Dana
; TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY
; FILE REFERENCE: P1867R1
; CURRENT APPLICATION NUMBER: US/10/227,694
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/315,209
; PRIOR PILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 1.
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Conservative:
Mismatches:
Indels:
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ORGANISM: Artificial sequence
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539.00
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84.13%
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COTHER INFORMATION: Synthetic
US-10-227-694-1
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-10-227-694-1
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Patent No. US200201419891

Patent No. US200201419891

GENERAL INFORMATION:

APPLICANT: Kricek, Franz

APPLICANT: Kricek, Franz

APPLICANT: Vogel, Monique

TITLE OF INVENTION: ANTIBODIES WHICH INHIBIT THE BINDING OF IMMUNOCLOBULIN E TO

TITLE OF INVENTION: ITS HIGH AFFINITY RECEPTOR

TITLE OF INVENTION: ITS HIGH AFFINITY RECEPTOR

TITLE OF INVENTION INMER: DS/09/974,449

CURRENT APPLICATION NUMBER: DCT/EPD0/03288

CURRENT PILING DATE: 2000-04-12

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FRRENCE: FRRENCE: A HIGHOMS VERBION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                       67 GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGGAGACAGAGTCACC 126
                                                                                                                                                                                                                                                                       187 GAGAAAGCCCCTAAGTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246
                                                                                                                                                                                                                                                                                                                              247 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 306
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                                                                                                                          21 AspileGlnLeuThrGlnSerProSerSerLeuSerAlaSerLeuGlyAspSerValThr
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61 GlyLysProProLysLeuValllePheAspGlySerIleLeuHisThrGlyValProSer
                                                                                                            CCTGGGGCTCCTGCTCTGTTTCCCAGGTGCCAGATGT
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106
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  104
16
23
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                                                                                 US-08-728-463B-208 (1-439) x US-09-800-729-150 (1-234)
 Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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Matches:
                                                      Gaps:
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                                                                                                            7 ATGGAGTTCCCCGTTCAGC
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540.50
95.00%
88.33%
545.00
83.92%
72.73%
68.90%
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141 SerAspGlu 143
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ORGANISM: Homo sapiens
US-09-974-449-36
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Best Local Similarity:
Query Match:
            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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LENGTH: 211
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CTGCAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGTACACT 357
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                                                                                                                                                                                                                                                                                                                                                                                                                          ZIE: 94000

ZIE: 94000

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/940,166A
FILING DATE: 27-Aug-2001
CLASSIPICATION - CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/097,309
FILING DATE: 13-UIN-1997
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106
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Fatent No. US20020058324A1
GENERAL INFORMATION:
Marindray, Dalit S.
Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSE:
ADDRESSES: Genentech, Inc.
STREET: 1 DNA MAY
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Schwartz, Timochy R. REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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                                                                                                                     418 TTCCCGCCATCTGATGAA 435
                                                                                                                                        INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
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539.00
90.48%
84.13%
68.14%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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178 CAGAAACCAGAGAAAGCCCCTAAGTCCTGATCTATTCTGCATCCAGTTGCAAAGTGGG 237
                                                                  CTGCAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGTACACT 357
                                                                                                                      TITGGCCAGGGGACCAAGCTGAGATCAAACGAACTGTGCTGCTGCACCATCTGTCTTCATC 417
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APPLICANT: MATSUKURA, SHIGEKAZU
APPLICANT: TSURUOKA, NOBUO
APPLICANT: ARIMA, KENJI
APPLICANT: ARIMA, KENJI
APPLICANT: NISHIHARA, TATSURO
TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
TITLE OF INVENTION: PLASMIDS THEREFOR
WUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-146-206C-25
PCT-US93-07832-25
US-08-1704-744-80
US-08-373C-39
US-08-437-642B-39
US-09-097-309-6
US-09-097-171A-10
US-09-460-587-6
US-09-460-587-6
US-09-460-587-6
US-09-460-587-6
US-09-460-11-945-52
US-08-452-164A-5
US-08-452-164A-5
US-09-460-587-6
US-09-97-171A-2
US-09-97-171A-2
US-09-97-171A-2
US-09-97-171A-2
US-09-109-207C-13
US-08-887-82
US-08-466-151-9
US-08-466-151-9
US-08-466-151-9
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US-08-466-151-9
US-08-463-587A-25
US-08-463-587A-25
US-08-463-587A-25
US-08-463-587A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PILLSBURY, MADISON & SUTRO STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NÜMBER: 35843
REFERENCE/DOCKET NÜMBER: 9437/204199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-157-101A-5; Sequence 5, Application US/08157101A; Patent No. 5808032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 202-861-37.
TELEFAX: 202-822-0944
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   Appl
Appl
                                                                                                  (without alignments)
2585.294 Million cell updates/sec
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Sequence 2, Ap
Sequence 14, A
Sequence 14, A
                                                                                                                                                                ATGGACATGGAGTTCCCCGT.......CCCGCCATCTGATGAAGCTT 439
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Sequence
                                                                                     3, 2003, 09:02:35 ; Search time 9.99241 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/jaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                            protein search, using frame_plus_n2p model
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US-08-812-586-16
US-09-042-353-48
US-08-812-586-45
US-08-08-53-131-185
US-08-096-762-185
US-08-217-918-2
US-08-25-372A-14
US-08-48-671-14
US-08-48-671-14
US-07-934-373C-25
US-08-48-671-14
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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791
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seq length: 200000000
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Match Length
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AGATGTGACATCCAGATGACCCAGTCTCCATCTCTCTGCATCTGTAGGAGACAGA 120
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61 LysProGlyGlnAlaProArgLeuLeuIleTyrAspAlaSerSerArgAlaThrGlyIle 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AAACCAGAGAAAAGCCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 48, Application US/09042353
Fatent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonbert M.
ITILE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,586
                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                        FILING DATE: 07-MAR.1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
FREFRENCE/DOCKET NUMBER: 0575/53862-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                      INFORMATION: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 235 amin
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584.00
85.52%
78.62%
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                                                                                                                                                                                                                          LENGTH: 235 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity:
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Patent No. 6048704
GENERAL INFORMATION:
APPLICANT: Martin David Tilson
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYM (AAA)
TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS: 61
ADDRESSEE: Cooper & Dunham Lip
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
CITY: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                     61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCACTGTCTGCATCTGTAGGAGACAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AAACCAGAGAAAGCCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATCAAGGTTCAGCGGCAGTGGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG
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                                                                                                                                                                           236
118
13
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                          US-08-728-463B-208 (1-439) x US-08-157-101A-5 (1-236)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 CCGCCATCTGATGAA 435
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TELEX: 6714627 CUCH
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acids
                                                                                                                                                                                      623.00
90.34%
81.38%
78.76%
                                                                                single
                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                             STRANDEDNESS:
                                                                                                                                                      Alignment Scores:
                                                                                                                          US-08-157-101A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-812-586-16
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DB:
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                                                                                                                                                                                      Score:
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235 114 10 21 0

LENGTH:

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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                     ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                   FILING DATE: 13-MAR-1998
CLASSIPICATION: 800
PRIOR APPLICATION DATA: 48 APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR ADDITE: 18-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRPLICATION NUMBER: US 07/904,068
FILING DATE: 23-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION NUMBER: US 08/053,131
APPLICATION NUMBER: US 08/053,131
APPLICATION NUMBER: US 08/056,762
APPLICATION UNMBER: US 08/096,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PALLICATION NUMBER: US 08/165,699
PILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-U1-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....בк: US 07/904,068
23-JUN-1992
ON DATA:
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PRIOR APPLICATION DATA:
APPLICATION NATA:
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                                                                                                                                 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : (415) 576-0300
FOR SEQ ID NO: 4
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                                                                                                                                                                                                                                                                            URRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
CORRESPONDENCE ADDRESS
                                                                                               California
                                                                                                                       USA
                                                                                                                  COUNTRY:
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240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                              21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 ValThrileThrCysArgAlaSerGlnGly1leSerSerTrpLeuAlaTrpTyrGlnGln
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                                                                                                                                                                                                                                                                                                         AAACCAGAGAAAGCCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                     1 ATGGACATGGAGTTCCCCGGTTCAGCTCCTGGGGGCTCCTGCTGCTGTTTCCCAGGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lonberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Fransgenic No. 6300129-Human Animals for Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                          117
111
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                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                  US-08-728-463B-208 (1-439) x US-09-042-353-48 (1-117)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
ELING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/728,463
                                                                                                                                                                                                                  Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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STATE: California
                                                                                                                          1.61e-58
578.00
96.58%
94.87%
73.07%
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: 117 amino acids
amino acid
3Y: linear
                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-042-353-48
                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-758-417A-313
                                                                                                         Alignment Scores:
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                                                                                                                          No.:
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RESULT 6
US-08-053-131-185
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Patent No. 6048704

GENERAL INCPEMATION:
APPLICANT: Martin David Tilson

IIILE OF INVENTION: PUBLIED AND RECOMBINANT ANTIGENIC

TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYM (AAA)

TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AGATGTGACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGGAGACAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AAACCAGAGAAAGCCCCTAAGTCCCTGATTCTGGATCCAGTTTGGAAAGTGGGGTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GTCACCATCACTIGICGGGCGAGICAGGGIATTAGCAGCTGGTTAGCCTGGTATCAGCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 CCATCAAGGTTCAGCGGCAGTGGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||||||||
| MetAppMetArgValLeuAlaGlnLeuLeuGlyLeuLeuLeuLeuCysPheProGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 CAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-728-463B-208 (1-439) x US-08-758-417A-313 (1-117)
                                                                                                                                                                                        NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41.303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
      US 08/209,741
                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 313;
                                                                                                                                                                                                                                       TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 313:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                             1.61e-58
578.00
96.58%
94.87%
                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                       US-08-758-417A-313
                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-812-586-45
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DB:
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133 TGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAA 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 GluLeuThrGlnSerProSerSerValSerAlaSerValGlyAspArgValThrIleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 AGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 AAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCGGCCATCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 TITGGAACTIATTACTGCCAACAGTATGATAGTTACCCGTACACTTTTGGCCAGGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 CAGATGACCCAGTCTCCATCTCACTGCATCTGTAGGAGACAGAGTCACCATC
                                                                                        COUNTRY: ...

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: BC-DOS/MS-DOS
OPTAME: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,586
FLING DATE: 07-MR-1997
CLASSIFICATION: 1435
ATTONENTY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 0575/53862-A
TELECOMMUNICATION INDMERR: 0575/53862-A
TELECOMMUNICATION 191-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-728-463B-208 (1-439) x US-08-812-586-45 (1-233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              TELBFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  573.00
96.69%
90.91%
72.44%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-812-586-45
                                                                           New York
(: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433 GAA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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82

42

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241 CCATCAAGGITCAGCGGCAGIGGAICIGGGACAGAITICACICICACCAICAGCAGCIG 300
                                                             Sequence 185, Application US/08096762
; Sequence 185, Application US/08096762
; Patent No. S814318.
; GENERAL INFORMATION:
    APPLICANT: Lonberg, Nils
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
                                                                                                                                            301 CAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTAC 348
                                                                                                                                                                               E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993
CLASSIPICATION BOOM
FILING DATE: 22-JUL-1993
CLASSIPICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 26-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/863,408
FILING DATE: 18-MRR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-MRR-1992
FILING DATE: 17-MRR-1992
FILING DATE: 17-MRR-1992
FILING DATE: 17-MRR-1992
FILING DATE: 17-MRR-1992
FILING DATE: 17-MRR-1992
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 14 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 185:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 116 amino acids
TYPE: amino acid
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96.55%
94.83%
72.19%
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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                                                                                  APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
UNMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 200 CITY: San Francisco CITY: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-728-463B-208 (1-439) x US-08-053-131-185 (1-116)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION BATA:
APPLICATION NATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTATION NUMBER: 14643-9-3
REFERENCE/DOCKET NUMBER: 14643-9-3
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
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TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMATION FOR SEQ ID NO: 185:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 185, Application US/08053131
Patent No. 5661016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.03e-57
571.00
96.55$
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amino acid
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                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                   121 GTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAG 180
                                                                                                                                                                                                                                                                   181 AAACCAGAGAAAGCCCCTAAAGTCCCTGATTTCTGCATCTGCAGTTTGCAAAGTGGGGTC 240
                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-08-259-372A-14
is Sequence 14. Application US/08259372A
j Patent No. 5565354
j GENERAL INFORMATION:
    APPLICANT: Ostberg, Lars G.
    TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
    TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
    TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
    TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
    TITLE OF INVENTION: AUTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
    NUMBER OF SEQUENCES: 16
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Twomsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, Eighth Floor
    CITY: San Francisco
                                                                                        1 ATGGACATGGAGTTCCCCGTTCAGCTCCTGGGGCTCCTGCTGCTGTTTCCCAGGTGCC
                                                                                                                                                                                                                        301 CAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGTACACTTTT
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: 14-JUN-1994
FLING DATE: 14-JUN-1994
CLASSIFICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION NUMBER: US 07/676,036
                               US-08-728-463B-208 (1-439) x US-08-217-918-2 (1-129)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 GGCCAGGGGACCAAGCTGGAGATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GlyGlnGlyThrLysValGluIleLys 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 27-MAR-1991
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
APPLICATION NUMBER: US 07/100-77811NUMBER: US 07/100-77811NUMBER: US 07/100-778711NUMBER: US 07/100-778711NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 06/904,517
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                 240
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                                     ATGGACATGGAGTTCCCCGTTCAGCTCCTGGGGCTCCTGCTGCTCTGTTTCCCAGGTGCC
                                                                                                                         AAACCAGAGAAAGCCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                          301 CAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTAC 348
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0; Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,918
FILING DATE: 24 MAR.1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,23
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 326-2400
INFORMATION FOR INFORMATION:
TELEFAX: (415) 326-2400
INFORMATION FOR INFORMATION:
TELEFAX: (415) 326-2400
INFORMATION FOR INFORMATION:
TELEFAX: (415) 326-2410
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
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108
112
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US-08-728-463B-208 (1-439) x US-08-096-762-185 (1-116)
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Matches:
Conservative:
Mismatches:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC. compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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83.72%
72.19%
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Best Local Similari
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us-08-728-463b-208.rai

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235 GGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGC 294
                                                                          295 AGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGTAC 354
                                                                                             ACTITIGGCCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTTC 414
                                                                                                                                                                     233
106
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13
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 18M PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                RESULT 12
US-064.47-642B-25
US-064.47-642B-25
Sequence 25, Application US/08437642B
Fatent No. 6054297
GENERAL INFORMATION:
APPLICANT: Leonard G. Presta
TITLE OF INVENTION:
TITLE OF INVENTION:
UNMERR OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING APPLICATION DATA:
APPLICATION NUMBER: 07/715272
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: 07/716272
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 03/818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P0709P2C1
                                                                                                                                                                                                                          415 ATCTTCCCGCCATCTGATGAA 435
                                                                                                                                                                                                                                              CORRESPONDED GENERAL ADDRESSEE: General STREET: 1 DNA Way CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650/225-1994
TELEPAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 233 amino acids
Amino Acid
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89.76%
83.46%
68.52%
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
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103 PheAlaThrTyrTyrCysGlnGlnAlaAspSerLeuProPheThrPheGlyGlyGlyThr 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 CAGCAGAAACCAGAGAAAGCCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 GGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCACTGTCTGCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUM-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 14-JUM-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709F2
TELECOMMUNICATION NUMBER: P0709F2
TELECOMMUNICATION NUMBER: P0709F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                            Sequence 25, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                          |||:::::: ||||||
123 LysValAspPheLysArg 128
                                       373 AAGCTGGAGATCAAACGA 390
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INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                               ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        542.00
89.76%
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68.52%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                            94080
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                                                                                                                            US-07-934-373C-25
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PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-UN-1994
APPLICATION NUMBER: US 07/871,426
PRIOR APPLICATION DATA:
APPLICATION DATE: US 07/676,036
FILING DATE: 27-MAR-1991
APPLICATION DATE: US 07/538,796
FILING DATE: 15-UN-1990
PRIOR APPLICATION DATA:
APPLICATION DATE: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1966
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
ATTORNEY AGENT INFORMATION:
NAME: SMICh, MILLIAM M.
REGISTRATION NUMBER: US 06/925,175
ATTORNEY AGENT INFORMATION:
NAME: SMICh, MILLIAM M.
REGISTRATION NUMBER: 30,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.13e-55
548.50
92.06%
84.92%
69,34%
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 TITGCAACTIATIACTGCCAACAGTATGATAGTTACCCGTACACTITTGGCCAGGGAAC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 cccorr -- caccrccracaccrccracracrarrrrccaagacacagargacarc 72
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08468671

Patent No. 548077

GENERAL INFORMATION:

APPLICANT: Ostberg, Lars G.

TITLE OF INVENTION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

ADDRESSER: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 GCCCCTAAGTCCCTGATCTATTCTGCATTTGCAAAGTGGGGGTCCCATCAAGTTC
                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                 US-08-728-463B-208 (1-439) x US-08-259-372A-14 (1-128)
                                                                                                                                                                                                                                                                   Length:
Matches:
ATTORNEY TORORATION:
NAME: Smith, William M.
REGISTRATION'NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 AAGCTGGAGATCAAACGA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                             548.50
92.06%
84.92%
69.34%
                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                              US-08-259-372A-14
                                                                                                                                                                                                                                             Alignment Scores:
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DB:
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73 CAGATGACCCAGTCTCCATCTGTGTGTGTGTAGGAGACAGAGTCACCATCACT 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 GCCCCTAAGTCCCTGATCTATTCTGCATCCAGTTGCGATGGGGTTCCATCAAGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128
107
9
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
Conservative:
Mismatches:
Indels:
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Alignment Scores:
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             Pred. No.:
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                                                                                                                                                                               175 CAGCAGAAACCAGAGAAAGCCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGT 234
                                                                                                                                                                                                                                                 235 GGGGTCCCATCAAGGTTCAGCGGCAGTGGGATCTGGGACAGATTTCACTCTCACCATCAGC 294
                                                                                                                                                                                                                                                                                                               295 AGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGTAC 354
                                                                16 GlyvalHisSerAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGly 35
                                                                                                                                355 ACTITIGGCCAGGGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25, Application US/08146206C

Patent No. 6407213

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

APPLICANT: Carter, Paul J.

APPLICANT: Dresta, Leonard G.

TILLE OF INVENTION: Method for Making Humanized Antibodies

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080
                                              GGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCT
             US-08-728-463B-208 (1-439) x US-08-437-642B-25 (1-233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWAKE: WITHEALTH (GENERICECT)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-NO. 6407213-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE TOOCKET NUMBER: P0709P1
TRIECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                   415 ATCTTCCCGCCATCTGATGAA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 233 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           650/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-146-206C-25
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115 GACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTAT 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 AGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGTAC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 ACTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTTC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 GGTGCCAGATGTCACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGGA
                                                                                                                                            US-08-728-463B-208 (1-439) x US-08-146-206C-25 (1-233)
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ZIP: 94080
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
TI.NG DATE: 19930820
                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRICE APPLICATION DATA:

APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION NUMBER: 07/934373
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415 ATCTTCCCGCCATCTGATGAA 435
2.79e-54
               542.00
89.76%
83.46%
68.52%
                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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175 CAGCAGAAACCAGAAAAGCCCCTAAGTCCTGATCTATTCTGCATCCAGTTTGCAAAGT 234
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||| GlyvalHisSerAspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGly 35
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Matches:
Conservative:
Mismatches:
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Gaps:
                                                                                             FILING DATE: 06-SEPT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/20886
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: PCT/US/95/02400
FILING DATE: 08-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: FOUlke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: 33,364
REFERENCE/DOCKET NUMBER: 38429K
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                             UMBER: US/08/704,744
06-SEPT-1996
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Job time : 12.9924 secs
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amino acid
GY: linear
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89.76%
85.04%
68.20%
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SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acid
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US-08-704-744-80
                                                    CURRENT APPLICATION DATA APPLICATION NUMBER:
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Best Local Similarity:
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Pred. No.:
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APPLICANT: Miller, Kenneth
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plonar Commentations of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation of the commentation 
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106
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Mismatches:
Indels:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
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Patent No. 5705154
GENERAL INFORMATION:
REGISTRATION NUMBER: 7.
REFERENCE/DOCKET NUMBER: 7.
TELECOMMUNICATION INFORMATION
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                    542.00
89.76%
83.46%
68.52%
                                                                                                     TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              : 233 amino ac
amino acid
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Best Local Similarity:
Query Match:
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                     PCT-US93-07832-25
                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-704-744-80
                                                                                                                                                                                                                 LENGTH:
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3, 2003, 08:56:26 ; Search time 22.1646 Seconds (without alignments) 4545.477 Million cell updates/sec
                                                                                                                                                                                                                         1 AAGCTTGCCACCATGAAACA.......GACTACTTCCCCGAACCGGT 524
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                     OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                             283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                    0.0
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0.0
0.0
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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967
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                                                                                                            June
                                                                                                                                                                                                         Perfect score:
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                                                                                                                                                                                                                           Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Command line parameters:
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-MODEL=frame+ n2p. model -DEV=xlp
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-DB=PIR 73 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-UNRM=spt -NORM=skt -HRAPSIZE=500 -MINIEN=0 -MAXLEN=200000000
-USER=US08728463 @CGN 1 1.77 @runat 03062003 085615 16827 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database

PIR_73:* 1: _pir1:* pir2:* pir3:* pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Ig heavy chain V r	Ig heavy chain pre	Ig gamma-1 heavy c	Id Fab region IV-J	Ig variable region	Ig heavy chain V4.	Ig heavy chain V r	Ig heavy chain V r	Iq heavy chain V r	Iq heavy chain V-I	Ig heavy chain - h	Iq heavy chain - h	Ig heavy chain V r	Id heavy chain pre
	ID	A49045	S78052	A49444	B23746	137782	S47010	S13519	S31676	S31586	B49028	831511 .	S31512	S31696	G1HUH2
	60	2	7	~	7	7	7	7	~	7	N	~	~	~	7
	Length	140	140	220	231	140	126	147	137	139	143	155	155	139	146
æ	Query re Match Length DB	70.2	66.1	62.9	62.5	62.4	61.4	61.0	60.1	60.1	59.9	59.8	59.6	59.3	59.2
	Score	629	639.5	608	604	603	593.5	590	581.5	581.5	579	578	576	573	572
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S78055	809711	B26340	PS0341	A24770	809710	A26340	S18557	JL0047	831673	831690	S31684	526898	831585	S78051	A41287	B41287	S14474	G34964	172667	E34964	S 54906	S26805	830530	S44114	531604	826806	JH0428	S22080	830529	8
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145	146	116	133	140	146	118	116	122	130	130	124	97	137	135	139	.143	97	97	114	117	134	97	123	129	135	97	97	470	123	97
58.9	57.3	56.9	56.7	56.0	55.9	55.7	55.6	54.8	54.3	54.3	53.7	53.6	53.4	53.4	53.0	52.8	52.6	52.5	51.7	51.4	50.9	50.7	50.7	50.5	50.3	49.9	49.9	49.2	49.1	48.8
569.5	554	550	548	542	541	539	538	530	525.5	525	519	518	516.5	Ω	\sim	510.5	ın	508	200		O)	a)	σ	488.5	9	483	483	475.5	475	472
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C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
E;Crillot-courvalin, C.; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silverm
Eur. J. Immunol. 22, 1781-1788, 1992
A;Title: An anti-18 cell autoantibody from Wiskott-Aldrich syndrome which recognizes i b
A;Reference number: A49045; MUD:9234290; PMID:1623923
A;Accession: A49045
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A;Accession: A49045 Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)

140 129 6 1 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 7.18e-50 679.00 93.57% 92.14% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: Pred. No.: Score:

US-08-728-463B-219 (1-524) x A49045 (1-140)

13 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCAGCTCCTAGATGGGTCCTGTCTCAG 72		73 GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 132	21 ValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeuThr 40
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	Oy 268 GTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTGTGAACTGAGCTCTGTGACC 327
	328 GCTGCGGACACGGCTGTGTATTACTGTGCGAGAGTAATTAAT
QY 253 TCTCTCAAQAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTGAAA 312	Db 101 AlaAlaAspThrAlaValTyrTyrCysAlaArgGlyGlySerValLeuArgPheLeuGlu 120 Qy 370 TGG
360	Db 121 TrpLeuLeuTyrProAlaPheAgpTyrTrpGlyGlnGlyThrLeuValThrValSerSer 140 RESULT 3
TCTCCTCA 414	Ig gamma-1 heavy chain (New) - human (fragment) C;Species: Homo sapiens (man) C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 16-Jul-1999 C;Accession: A9444
agment) -Jul-1999	R;Saul, F.A.; Poljak, R.J. Proteins 14, 363-371, 1992 A;Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A re: A;Reference number: A49444, MUID:93066153; PMID:1438175 A;Ccession: A49444
	A; Stacus: preintary A; Mocaule type: protein A; Residues: 1-220 < SAU> A; Note: sequence modified after extraction from NCBI backbone A; Note: sequence report includes corrections based on crystal structure refinement C; Suberfamily: immunocalchilin C region: immunocalchilin benefit
910118	C; Keywords: immunoglobulin F;137-202/Domain: immunoglobulin homology < IMM>
R; Harindranath, N.; Goldfarb, I.S.; Ikemateu, H.; Burastero, S.E.; Wilder, R.L.; Notkins Int. Immunol. 3, 865-875, 1991 A; Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h patient. A; Reference number: S23716; MUID:92031262; PMID:1718404 A; Accession: S23777	Alignment Scores: 7.79e-44 Length: 220 Pred. No.: 608.00 Matches: 115 Score: 608.00 Matches: 115 Bercent Similarity: 86.93 Conservative: 18 Best Local Similarity: 75.16 Mismatches: 18
A; Residues: 15-11 - ABM> A; Cross references: EMBL:X54441 C; Superfamily: imminoglobilin V region: imminoglobility	3B-219 (1-524) x A49444 (1-220)
C.Keywords: immunoglobulin F:1-14/Domain: signal sequence (fragment) #starus predicted <sig> F:15-114/Domain: signal sequence (fragment) #starus predicted <sig> F:25-14/Product: Ig heavy chain (fragment) #status predicted <mat></mat></sig></sig>	Qy 70 CAGGTGCAGCTACAGCAGTGGGGGGGGGGGGTGTTGAAGCCTTCGGAGACCCTGTCCCTC 129
Alignment Scores: Pred. No.: 1.63e-46 Length: 140 Score: 639.50 Matches: 124	<pre>Qy 130 ACCTGCGCTGTCATAGGTGGTTACTACTGGAGCTGGATCGCCAGCA 189</pre>
Beet Local Similarity: 90.004 Conservative: 2 Query Match: 66.134 Indels: 11 DB: 2 Gaps: 2	<pre>Qy 190 CCAGGTAAGGGTCTGGAGTTGGTGAAATCAATCATAGTGGAAGCACCAACTACAAC 249</pre>
	Qy 250 CCGTCTCTCAAGAGTCGAGTCACATATCAGTAGACCAGGAACCAGTTCTCTCTG 309 Db 61 ProSerLeuArdGlvArcValThrWarlanValBanThrCarlan
. H	310 AAACTGAGCTCTGTGACCGCTGCGACACGGCTGTGTATTACTGTGCGGAGAGTA
QY 88 TGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCCTCCCCCCCGCGCTGTCTATGGT 147 Db 21 TrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeuThrCysAlaVallyrGly 40	Db 81 ArgleuSerSerValThrAlaAlaAspThrAlaValTyrTyrCygAlaArgAsnLeuIle 100 Qy 364 ATTAATTGGTTCGACCCTTGGGGCAACCCTGGTCACCTCTCTCT
OY 148 GGTTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCA	Db 101 AlaGlyGlyIleAbValTrpGlyGlnGlySerLeuValThrValSerSerAlaSerThr 120 Oy -424 AAGGGCCCATCGGTCTTCCCCTGGCACCTCCTCCAAGAGACACTTGAAGACAAAAAAAA
208	
Db 61 Trp11eGlyGlu11eAsnH1sSerGlySerThrAsnTyrAsnProSerLeuLysSerArg 80	Qy 484 GCCTGGGCTGCTGGTCAAGGACTACTTCCCCGAACGG 522

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antibody
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            A;Molecule type: mRNA
A;Residues: 1-140 <RES>
A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;46-128/Domain: immunoglobulin homology <IMM>
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C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: 137782; S25476
Fx:Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Status: preliminary
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: B2346
R;Leoni, J; Ghiso, J; Goni, F; Frangione, B.
J, Biol. Chem. 266, 2836-2842, 1991
J, Filen: The primary structure of the Fab fragment of protein KAU, a monoclo A;Title: The primary structure of the Fab Fragment of protein KAU, a monoclo A;Tatus: preliminary
A;Accession: B23746
A;Actus: preliminary
A;Rolecule type: protein
A;Reference numbor: A23746
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956	Data Library, June 1992 Smms that generate human immunoglobulin diversity 1585 Bizzi 1882; NID: 931031; PIDN: CAA78551.1; PID: 9310 Inbulin V region; immunoglobulin homology aner; immunoglobulin homology < IMM>
C. Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999 C; Accession: 813519 R; Mortari, F.; Ochs, H.D; Wedgwood, R.J.P.; Schroeder Jr., H.W. Nucleic Acids Res. 19, 673, 1991 A; Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked A; Accession: 813519; MUID:91187691; PMID:2011536 A; Accession: 813519 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-147 < MOR> A; Residues: Efferences: EMBL:X56158; NID:937724; PIDN:CAA39626.1; PID:g37725 C; Superfamily: immunoglobulin V region; immunoglobulin homology	Alignment Scores: Pred: No.: Score:
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143 3 3 4 114 3 3 4

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73 GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 132
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C;Species: Homo sapiens (man).
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31511
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of A;Reference number: S31509
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579.00
83.57%
81.43%
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-155 < CHA>
                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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S31511
Ig heavy chain - human
                          Scores:
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: J1.2352343
C;Accession: B49028
R;Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur
Eur. J. Immunol. 21, 2355-233, 1991
A;Tile: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A;Reference number: A49028; MUID:92008140; PMID:1915549
A;Retence number: A49028
A;Status: preliminary
A;Molecule type: mRNA
A;Status: preliminary
A;Molecule type: mRNA
A;Reterences: GB:S6473; NID:9236906; PIDN:AAB20012.1; PID:9236907
A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:64473, NCBIP:64472)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterzamer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31586
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Description: Mechanisms (231586
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-139 cCUI>
A;Cross-references: EMBL: Z14196; NID:930978; PIDN:CAA78565.1; PID:930979
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Superfamily: immunoglobulin homology cIMM>
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anti-DNA

Db 94 ProlleLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLys 113 Qy 313 CTGAGCTCTGTGCGCACCGCTGCTGTATTACTGTGGAAGTA 363 :::	RESULT 13 \$31656 Ig heavy chain V region - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999 C;Accession: 831696 R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992 A;Reference number: 831886 A;Reference number: 831886 A;Accession: 831696 A;Accession: 831696 A;Accession: 1-139 CUI A;Residues: 1-139 CUI A;Cross-references: EMBL:214194; NID:930975; PIDN:CAA78563.1; PID:930976 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin Norelogion of Norelogy C;Superfamily: immunoglobulin homology clm> F;34-116/Domain: immunoglobulin homology clm>	ignment Sco: ed. No.: ore: rcent Simils st Local Sir ery Match: :	Oy 13 ATGAAACACTGTGGTTCTTCCTCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCG 72 1	Db 41 CysThrValSerGlyGlySerIleSerSerTyrTyrTrpSerTrpIleArgGlnProAla 60 Qy 193 GGTAAGGGTCTGGAGTTGGTGAAATCAATCAATGTGGAAGCACCAACTACAACCG 252 Db 61 AlaLysGlyLeuGlUTrpIleGlyArglIeTyrThrSerGlySerThrAsnFyrAsnFro 80 Qy 253 TCTCTCAAGAGTCGACATACACCATACAAGAACCAGTTCTTGAAA 312	Db 81 SerieulysSerArgValThiMetSerValAspThrSerLysAsHollH
. 34 133 193 193 253	0y 313 CTGAGCTCTGTGACGCTGCGAACACGCCTGTATTACTGTGCGAGAGTA 363 bb 114 vaisErSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlyGlyGlyIle 133 0y 364 ATTAATTGGTTC	Submitted to the EMBL Data Library, December 1992 A; Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autc A; Reference number: \$31509 A; Reference number: \$31512 A; Status: preliminary A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-155 cGHA> A; Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin homology cIMA> F; 47-129/Domain: immunoglobulin homology cIMA>	Alignment Scores: 4.06e-41 Length: 155 Score: 576.00 Matches: 111 Percent Similarity: 78.17\$ Mismatches: 14 Query Match: 59.57\$ Indels: 2 Gaps: 2	US-08-728-463B-219 (1-524) x S31512 (1-155) Oy	TGCGCTGTTATGGGGGTTCCTTCAGTGGTTACTACTGGGGCTGGATCCGCC? TGCGCTGTCTATGGGGGTTCCTTCAGTGGTTACTACTGGGGTCGGATCGCCCC? CYSThrValSerGlyGlySerIleSerSerTyrTyrTrpSerTrpIleArgGl GGTAAGGGTCTGGAGTGGATTGGTGAAATCAATCATAGTGGAAGCACCAACTA [

from the

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Ig heavy chain precursor V-D-J region (clone mAB 67VH) - human (fragment)
C;Species Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: 878055; 823720
R;Harindranath, N.
S:Marindranath, N.
A;Accession: 878051
A;Accession: 878055
A;Accession: 878055
A;Accession: 878055
A;Accession: 878055
A;Accession: 878055
A;Accession: 878055
B;Hashidranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin: R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkin: A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and i
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Job time: 24.1646 secs
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C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-146/Product: Ig heavy chain V-II region (ARH-77) #status predicted <WAT>
F;20-117/Region: V segment
F;35-117/Domain: immunoglobulin homology <IMM>
F;118-1127/Region: J segment
F;128-146/Region: J segment
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A;Gene: GDB:IGHV@
A;Gene: GDB:IGHV@
A;Gene: GDB:128528; OMIM:147070
A;Map Position: 14432.33-14432.33
A;Introns: 16/3
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F;42-115/Disulfide bonds: #status predicted
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X MODINE-85205332; PubMed=3922855;

X Kudo A., Ishihara T., Nishimura Y., Watanabe T.;

X Loned human immunoglobulin heavy chain gene with a novel direct-repeat sequence in S' flanking region.";

I A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequence in S' flanking region.";

I A A02101; GlHUH2.

R INSP: PO1825; PAPAB.

R InterPro; IPR003066; Ig_WHC.

InterPro; IPR003596; Ig_V.

R Pfam; PF00047; ig; 1.

R MART; SM00406; IGV, 1.

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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V.II region ARH-77 precursor.
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-MODEL=frame+ n2p.model -DEV=xlp
-Q=/CGR12_1/USFTO spool/US08728463/runat_03062003_085614_16804/app_guery.fasta_1.3690
-DB=SwisSProt_40_CFMT=fastan -SUFFIX=rsp -MINMATCH=0.1_-LOOPCL=0_-LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blooum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM==ext -HEAPSIXE=500 -MINLEN=20000000000
-USRS=US08728463_@CGN 1 1.76_@runat_03062030_365614_16804_NCFU=6_-ICFU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-NOW_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                  - protein search, using frame_plus_n2p model
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130 ACCTGCGCTGTCTATGGTGGTTCCTTC----AGTGGTTACTACTGGAGCTGGATCCGC 183
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G heavy chain V-II region NEWM.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
MEDLINE-78066916; PubMed=618887;
Saul F.A., Amzel L.M., Poljak R.J.;
"Preliminary refinement and structural analysis of the Fab fragm from human immunoglobulin new at 2.0-A resolution.";
J. Biol. Chem. 253:585-597(1978).
--- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
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INDEATPO; 1PR003006; 1G_MC.

INTEATPO; 1PR003596; 1G_V.

Pfam; PF00047; 1g; 1.

IMMART; SM00406; IGV; 1.

IMMART; SM00406; IGV; 1.

IMMART; SM00406; IGV; 1.

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IMMART; SM00406; IGV; 1.

IMMART; SM00406; IGV; 1.

PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=77242302; PubMed=407927;
Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
"Amino acid sequence of the VH region of a human myeloma immunoglobulin (IgG New)";
                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA
                       US-08-728-463B-219 (1-524) x HV2F_HUMAN (1-129)
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Biochemistry 16:3412-3420(1977).
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                          13 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCTAGA---TGGGTCCTGT
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.
"Complete amino acid sequence of the delta heavy chain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D5D53D47ABE51319 CRC64
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Mismatches:
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V-II region WAH.
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US-08-728-463B-219 (1-524) x HV2I_HUMAN (1-146)
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PIR; A02099; DZHUWA.
HSSP; P01825; 7FAB.
GlycoSulteDB; P01824;
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_V.
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62.02%
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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Best Local Similarity:
Query Match:
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13 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAG 72
Jilka R.L., Pestka S.; "Amino acid sequence of the precursor region of MOPC-315 immunoglobulin heavy chain.";
                                       SEQUENCE OF 1-21.
MEDLINE-79148758; PubMed=428562;
Schechter I., Wolf O., Zemell R., Burstein Y.;
"Structure and function of immunoglobulin genes and Fed. Proc. 38:1839-1845(1979).
                       Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
NCBI_TaxID=10090;
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the rearranged MOPC 315 VH
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01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
pheavy chain V region MOPC 315 precursor.
Mus musculus (Mouse)
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SEQUENCE FROM N.A.
MEDLINE=89238351; Pubmed=2497341;
Rinfret A., Horne C., Dorrington K.J., "Cloning, sequencing and expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE OF 1-31.
MEDLINE=78094475; Pubmed=414225;
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Mol. Immunol. 26:431-434(1989)
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81.20%
64.96%
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Best Local Similarity:
 gene segment
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
MEDLINE=74170779; PubMed=4524622; Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.; Mamino-acid sequence of the variable region of the heavy (alpha) chain of a mouse myeloma protein with anti-hapten activity."; Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
                                                                                                                                                                             MEDLINE=77244979; PubMed=268248;
Hood L., Margolies M.N., Givol D., Zakut R.;
Unpublished results, cited by:
Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
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FRAMEWORK-1.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
G -> G (IN REF. 1; CAA30727).
G -> H (IN REF. 2).
GY -> YG (IN REF. 4).
N -> D (IN REF. 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M7638; AAA6137.1; ---
EMBL; X07880; CAA30727.1; ---
PIR; PL0102; AVMS35.
HSSP; P01825; 7FAB.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR00306; Ig_V.
Ffam; PF00047; ig; 1.
SWART; SM00406; IGV.
Immunoglobulin V region; Signal.
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MM.
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393.50
73.19%
59.42%
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GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 132
                                                                                                                                                                        133 TGCGCTGTCTATGGTGGTTCCTTC---AGTGGTTACTACTGGAGCTGGATCCGCCAGCCA 189
                                                                                                                                                                                                                                                                                    249
                                                                                                                                                                                                                                                                                                                                                                    CCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGGACACGTCCAAGAACCAGTTCTCTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCG------AGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||||:::||||||||||
LysLeuAsnSerValThrTluAspThrAlaThrTyrTyrCysAlaGlyAspAsnAsp 119
|||:::||| ||| ||| ||| CysSerIleThrSerGlyTyrPheTrpAsnTrpIleArgGlnPhe 59
                                                                                                                                                                                                                                                                                                                                   79
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|ProGlyasnLysLeuGluTrpLeuGlyPheIleLysTyraspGlySerasnGlyTyrasn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 GTAATTAATTGGTTCGACCCTTGGGGCCAGGGAACCCTGGTCACCGTCTCTCA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 HisbeulyrTyrPheAspTyrTrpGlyGlnGlyThrThrLeuThrValSerSer 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during U.S.P. Med. 169:2007-2019(1989).
J. Exp. Med. 169:2007-2019(1989).
PIR; JT0509; HVMS31.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_V.
Pfam; PF00047; ig; 1.
PMRRT; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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PRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116
13095 MW; 4562E03E53DC9E10 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/CJ;
MEDLINE=89279149; PubMed=2499654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.47e-24
370.00
76.92%
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Pred. No.:
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DOMAIN
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Percent Similarity: Best Local Similarity:

Query Match: DB:

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                                                                                             GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 132
                                                                                                                                                           133 TGCGCTGTCTATGGTGGTTCCTTC---AGTGGTTACTACTGGAGCTGGATCCGCCAGCCA 189
                                                                                                                                                                                                                                249
                                                                                                                                                                                                                                                                                      CCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTG 309
                                                   |||||||
60 ProGlyAsnLysLeuGluTrpWetGlyTyrlleSerTyrAspGlySerAsnAsnTyrAsn 79
                                                                                                                                                                                                                                                                                                           13 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCAGCTCCTAGATGGGTCCTGTCTCAG
                                                                                                                                                                                                                        CCAGGTAAGGGTCTGGAGTGGATTGGTGAAATCAATCATAGTGGAAGCACCAACTACAAC
                                                                                                                 MEDLINE=81012133; PubMed=6774258; Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.; Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.; Tuo of somatic recombination are necessary for the generation of complete immunoglobulin heavy-chain genes."; Nature 286:676-683 (1980).

-I- MISCELLANBOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A DIFFERENTIATED GENE ISOLATED FROM A MYELOWA THAT SECRETES IGG2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                    AAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCGAGA 360
                                                                                                                                                                                                                                                                                                                                                                        IG HEAVY CHAIN V REGION MOPC 141,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15759 MW; 8E47A7CB3:706D30A CRC64
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74
22
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
18 heavy chain V region MOPC 141 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 AA
US-08-728-463B-219 (1-524) x HV60_MOUSE (1-116)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, V00768; CAA24149.1; -. PIR; AA2044; G2MS14. HSSP, P01825; 7FRB. InterPro; IPR003506; Ig_WHC. InterPro; IPR003596; Ig_V.
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358.00
66.67%
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxiD=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 HV43 MOUSE
P01819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                               73
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21 ThrCysSerValThrGlyAspSerlleThrSerAspTyrTrpAsnTrpIleArgLysPhe 40
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                                                                                                                                                                                                                                                                                                                                                                  61 ProSerLeuLysSerArglleSerIleThrArgAspThrSerLysAsnGlnTyrTyrLeu 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A DIAMES BALDY, The BALDY, Malipiero U.V., Lebecque S.G., Gearhart P.J.;
A Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
The primary immune response.":
J. Exp. Med. 169:2007-2019 (1989).
C -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
R PIR, JT0508; HVWS1B.
R INTERPROS POUSES; 7FAB.
R INTERPROS IPRO03006; Ig_WC.
R RINTERPROS IPRO03006; Ig_V.
R SMART; SM00406; IGV; 1.
M Immunoglobulin V region; Signal.
                                                                                                                                                                            CCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                70 CAGGIGCAGCIACAGCAGIGGGGCGCAGGACTGTIGAAGCCTICGGAGACCCTGTCCCTC
                                                                                                                                                                                                                                                                                  190 CCAGGTAAGGGTCTGGAGTGGATTGGTGAAATCAATCATAGTGGAAGCACCAACTACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 TGGTTCGACCCTTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 ArgPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAla 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG HEAVY CHAIN V REGION 1B43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW; 1CB547253681FF74 CRC64;
                 113
70
20
23
23
                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region 1B43 precursor.
Mus musculus (Mouse).
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BY SIMILARITY
                                                                                                                             US-08-728-463B-219 (1-524) x HV47_MOUSE (1-113)
                                                                                                 Gaps:
                              354.00
78.26%
60.87%
36.61%
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48
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                                               Percent Similarity:
Best Local Similarity:
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   Alignment Scores:
Pred. No.:
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P18532;
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MetAsnSerLeuGlnThrAspAspThrAlaArgTyrTyrCysAlaSerValSerIleTyr 120
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                                                                                                                                                          GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 132
                                                                                                                                                                                                                      193 GGTAAGGGTCTGGAGTGGATTGGTGAAATCAATCATAGTGGAAGCACCAACTACAACCCG 252
                                                                                                                                                                                                                                                                                                                                                                                                              72
                                                                                                                           20
                                                                                                                                                                                       40
                                                                                                                                                                                                                                                                                                  61 GlyLysGlyLeuGluTrpLeuGlyThrIleTrpGlyAsnGlySerThrAspTyrAsnSer 80
                                                                                                                -!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF STRIN A/J MICE.
                                                                                            ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAG
                                                                                                                                                                                                                                                                                                                                              TCTCTCAAGAGTCGAGTCACATATCAGTAGACACGTCCAAGAACCAGTTCTCTCTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTC-------GACCCTTGGGGCCAGGGAACCCTGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=A/J;
MEDLINE=84024551; PubMed=6414509;
Juszczak E.C., Margolies M.N.;
"Amino acid sequence of the heavy chain variable region from the mouse anti-arsonate monoclonal antibody 36-60 bearing a minor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 AA; 12734 MW; 38DC0E0E3F5075B7 CRC64;
    38
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SMART; SM00406; IGv; 1.
Immunoglobulin v region; Antiarsonate antibody.
SEQÜENCE 113 AA; 12734 MW; 38DC0E0E3F5075B7
Mismatches:
Indels:
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-PUL-1999 (Rel. 38, Last annotation update)
                                                               US-08-728-463B-219 (1-524) x HV43_MOUSE (1-144)
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HSSP; P01825; 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
51.39%
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 Best Local Similarity:
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                 Query Match:
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84 ValThrIleThrLysAspAsnGlyLysLysGJnValTyrLeuGlnMetAsnGlyMetGlu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 ValLysAspThrAlaMetTyrTyrCysAlaArgGluTyrAlaSerGlyTyrAsnPheAsp 123
                                                                                                                                                                                                                                                                                   28 ITCITCCTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAGGTGCAGCTACAGCAG
                                                                                                                                                                                                                                                                                                                                                24 SerGlyProGlyThrValLysProSerGluSerLeuArgLeuThrCysThrValSerGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
PIR; JT0510; HVMS73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090;
                               IG HEAVY CHAIN V REGION XIG14.
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                                                               EBC467105C00732E CRC64;
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70
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Mismatches:
Indels:
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01-NOV-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
11g heavy chain V region 733 precursor.
Mus musculus (Mouse).
                                                                                                                 Length:
Matches:
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                                                             15080 MW;
                                                                                                                 2.84e-21
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InterPro, IPR003006, 1g_MHC.
InterPro, IPR003596, 1g_V.
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Best Local Similarity:
Query Match:
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                                                                                           Alignment Scores:
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                            CHAIN
NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                 TGCGCTGTCTATGGTGGTTCCTTC---AGTGGTTACTACTGGAGCTGGATCCGCCAGCCA 189
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|ProGlyAsnLysLeuGluTrpWetGlyTyr1leHisTyrSerGlyAsnThrSerTyrAsn
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 AAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCGAGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88176921; PubMed-2451244; Schwager J., Mikoryak C.A., Steiner L.A.; "Amino acid sequence of heavy chain from Xenopus laevis IgM deduc from cDNA sequence: implications for evolution of immunoglobulin
                      116
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71
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01-FEB-1991 (Rel. 17, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
19 heavy chain v region XIG14 precursor (Fragment)
Xenopus laevis (African clawed frog)
                   Length:
Matches:
Conservative:
Mismatches:
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InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
NON_TER
              7.08e-22
343.00
74.36%
60.68%
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                                           Percent Similarity:
Best Local Similarity:
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Alignment Scores:
Pred. No.:
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P20957;
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DB:
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307 CTGAAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCGAGAGTA--- 363
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|LeuGlnMetSerLysValArgSerGluAspThrAlaLeuTyrTyrCysAlaArgLeuGly 100
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MEDLINE-84248078; PubMed-6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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"Illegitimate recombination generates a class switch from C mudelta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168 (1984).
PRS. A02033; HVMSTY.
HSSP; P01810; 2FBJ.
InterPro; IPR003596; Ig_W.
Fram; PP00047; ig, Illegion; Signal.
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FRAMEWORK-4.
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     Conservative:
Mismatches:
Indels:
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23-OCT-1986 (Rel. 02, Last sequence update)
24-UUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region TEPC 1017 precursor.
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                                                                                    US-08-728-463B-219 (1-524) x HV38_MOUSE (1-119)
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138 AA;
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P03980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
"Structural evidence for independent joining region gene in
"Structural evidence for independent joining region gene in
immunoglobulin heavy chains from anti-galactan myeloma proteins and
its potential role in generating diversity in
complementarity-determining regions.";
Proc. Natl. Acad. Sci. U.S. 76. 2899-2894 (1979).
--- MISCELLANBOUS: THIS CHAIN WAS ISOLATED PROM AN IGA MYELOMA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                              CTGAAACTGAGCTCTGTGACCGCTGCGGCTGTGTGTTTACTGTGCGAGA 360
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                    13223 MW; 1595517827F976BE CRC64;
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65
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region T601.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 AA
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Matches:
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119 AA; 13169 MW;
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PIR, A02078; AVMST6.
HSSP; PO1810; 2FBJ.
INTERPRO; IPR003006; IG MHC.
INTERPC; IPR003596; IG_V.
Ffan; PF00047; IG_V.
SWART; SM00406; IGV; I
                                                             1.82e-20
326.50
70.34%
57.63%
33.76%
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117 AA;
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                                                                                                                                                                      85 CAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTAT 144
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105 LeuThrProGluGluPheAlaValTyrTyrCy8AlaArgSerAspGlyTyrTyrAspTrp 124
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                                                                                                                                  GAGTGGATTGGTGAAATCAAT - - - CATAGTGGAAGCACCAACTACAACCGTCTCTCAAG
                                                                                                                                                                                                                                                                                                          262 AGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTCTGAAACTGAGCTCT
                                                                                                                                                                                                                                                                                                                                                                  "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HV07 MOUSE STANDARD; PRT; 139 AA.
PR0751, P01752;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 heavy chain V region B1-8/186-2 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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               Conservative:
Mismatches:
Indels:
    Matches:
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MEDLINE=81234548; PubMed=6788376;
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326.00
67.16%
49.25%
33.71%
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         Percent Similarity:
Best Local Similarity:
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                                                        IG HEAVY CHAIN V REGION B1-8/186-2. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2. COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3.
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Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae; Mus
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SEQUENCE FROM N.A.
MEDIJINE=83021113; PubMed=6181731;
Auffray C., Sikorav J.L., Ollo R., Rougeon F.;
"Correlation between D region structure and antigen-binding specificity: evidences from the comparison of closely related
                                                                                                                                                                        15419 MW; 1B57DD4FD0C9F465 CRC64;
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Matches:
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Mismatches:
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
18 heavy chain V region UPC10.
Mus musculus (Mouse).
                                                                                                                                                  BY SIMILARITY.
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JH2 SEGMENT
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           Pfam; PF00047; ig; 1... SMART; SM00406; IGv; 1.:
Immunoglobulin V region; Signal.
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InterPro; IPR003596; Ig_v.
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67.42%
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                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Ann. Immunol. (Paris) 132D:77-88(1981).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG GAMMA-2A MYELOMA
PROTEIN BINDING 2,6-LEVAN.
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19-0438;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1998 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 heavy chain V-II region SESS precursor.
Homo saplans (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B20A1074F8E99E7F CRC64;
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Matches:
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SEQUENCE FROM N.A.
MEDLINE=84298107; PubMed=6089186;
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94 GCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTATGGTGGTTCC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 LeuThrIleSerLysAspThrSerLysAsnGlnValValValLeuLysValThrAsnMetAsp 107
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||| TrpLeuAlaArgIleAspIrpAspAspAspLysTyrGlyThrSerLeuGluThrArg
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Takahashi N., Noma T., Honjo T.; "Rearranged immunoglobulin heavy chain variable region (VH) pseudogene that deletes the second complementarity-determining
                                                                                                                                                                                                                                        IG HEAVY CHAIN V-II REGION SESS. V SEGMENT. D SEGMENT. J SEGMENT.
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                                                                                                                                                                                                                                  20 147 IG HEAVY CHAIN V-II REGLOUS 20 118 V SEGMENT. 119 132 D SEGMENT. 147 J SEGMENT. 147 AA; 16323 MW; FCBCDB3D00FB6666 CRC64;
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71
17
139
14
                                                                 Progr. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984)
PIR; A02090, G2HUCS.
HSSP; PO1825, 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
SMART; SM00406; IGy.
Immoglobulin V region; Signal.
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Matches:
Conservative:
Mismatches:
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62.41%
50.35%
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Best Local Similarity:
Query Match:
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Q8tc63 homo s
Q96kx8 homo s
Q95kx8 homo s
Q9573 homo s
Q99m22 mus m
Q99m173 homo s
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Q8vea0 mus m
Q91z07 mus m
Q96ga6 homo s
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Q9ul75 homo e
Q99ka4 mus m
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Q924p8 mus n
Q96dk0 homo s
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Q991a6 mus
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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TISSUE=LYMPH,
Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC019235, AAH19235.1;
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003506; Ig.MHC.
InterPro; IPR003506; Ig.MHC.
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Last annotation update)
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               Q9BQBB
Q8TC63
Q8TC63
Q96KXB
Q95573
Q99M27
Q99L77
Q99L71
Q99L31
Q8VCX7
Q99LC4
Q91X92
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Q91WR1
Q8VCX4
Q9UT5
Q99KA4
Q8WT38
Q91XE1
Q8VCV5
Q8VEQO
Q91ZQ7
Q8VEAQ
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                                                                                  (Human)
NCBI_TaxID=9606;
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504.5
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                                                                                                           1 AAGCTTGCCACCATGAAACA......GACTACTTCCCCGAACCGGT 524
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        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                      OM nucleic - protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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01-UNA-2001 (TrEMBLrel. 17, Last sequence update)

01-UNA-2001 (TrEMBLrel. 17, Last sequence update)

01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Hypotherical 65.3 kDa protein.

Homo sapiens (Human).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
SWART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
Hypothetical protein.
SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;
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TISSUB-LYMPH;
Straudborg R.;
Submitted (EBB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002963; AAH02963.1;
HSSP; P01825; 7FAB.
                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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InterPro; IPR003597; 19 cl.
InterPro; IPR003600; 19_like.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 67.8 kBa protein.
Homo sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                 al protein.
597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
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Matches:
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig, 5.
SMART; SM00409; IG; 2.
SWART; SM00400; IGC; 1, 4.
SWART; SM00406; IGV; 1.
SMART; SM00410; IG like; 1.
SMART; SM00410; IG like; 1.
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SEQUENCE FROM N.A.
TISSUE=LYMPH;
Strausberg R.;
                                                                                                                                                                                                                                                                                          Hypothetical
SEQUENCE 59
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AC 096AA
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GGTAAGGGTCTGGAGTGGATTGGTGAAATCAATCATAGTGGAAGCACCAACTACAACCCG 252
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                                                                                             InterPro; 1PR00359; IG.
InterPro; 1PR00359; Ig.
InterPro; 1PR003597; Ig.cl.
InterPro; 1PR003006; Ig.Mc.
InterPro; 1PR003006; Ig.Mc.
InterPro; 1PR003096; Ig.V.
Pfam; PP00047; Ig. 5.
SMART; SM00407; IG.2.
SMART; SM00407; IG.2.
SMART; SM00410; IG.1; 4.
SMART; SM00410; IG.1; 4.
SMART; SM00410; IG.1; 1.
SMART; SM00410; IG.Mc; UNKNOWN 3.
PROSITE; PS00290; IG.Mc; UNKNOWN 3.
SEQUENCE 597 AA; 65300 Mw; 2DĀPAD50A6375851 CRC64;
                                                  EMBL/GenBank/DDBJ databases
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Matches:
Conservative:
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                                      Strausberg R.;
Submitted (JAN-2001) to the J
EMBL, BC06180; AAH06180.1;
EMBL, BC001872; AAH01872.1;
HSSP; P01825; 7FAB.
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Best Local Similarity:
Query Match:
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GJUN-2001 (TrEMBLrel. 17, Created)

01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Unknown (protein for MGC:1905) (protein for MGC:1228).

Homo sapiens (Human).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC017356; AMH17356.1; -. InterPro; IPR03598; Ig c2. InterPro; IPR003508; Ig mHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=MUSCLE;
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                            Pfam; PF00047; ig; 5. 5. 5. 8MART; SM00408; IGG2; 1. PROSITE; PS00290; IG_MHC; UNKNOWN 3. Hypochetical protein; Immunoglobulin domain. SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;
                                                                                                                                    Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                        187 CCACCAGGTAAGGGTCTGGAGTGGATTGGTGAAATCATAATGTGGAAGCACCAACTAC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 AACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCT 306
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108 LeulysLeuAspSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaAlaGlyHis 127
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                                                                                                                                                                                                                                                                                                                                                                                                 48 CysthrvalSerdlyAspServalAlaSerSerSerTyrTyrTrpGlytrpValArgdin 67
                                                                                                                                                                                                                                                                                                                                                                                                                                       68.ProProGlyLyBGlyLeuGluTrpIleGlyThrIleAsnPheSerGlyAsnMetTyrTyr 87
                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                 13 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GTAATTAATTGGTTCGACCCTTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (protein for MGC:20337).
Homo asplans (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalía; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGCGGCCCTGGCTGGTCAAGGACTACTTCCCCCGAACCG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 182
                                                                                                              Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025985; AAH25985.1; -.
Hypothetical protein.
SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
   Last annotation update)
                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                            US-08-728-463B-219 (1-524) x Q8TC63 (1-473)
01-JUN-2002 (TrEMBLrel. 21, Lar
Hypothetical 52.0 kDa protein.
Homo sapiens (Human)
                                                                                                                                                                                6.91e-57
655.50
81.14%
73.71%
67.79%
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                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                            SEQUENCE FROM N.A.
TISSUE=KIDNEY;
                                                                                                    Strausberg R.;
                                                                                                                                                                    Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 TCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTGAAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 SerLeulysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSerLeulys 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 GCCTCAACCAAGGGCCCCATCGGTCTTCCCCTTGGCACCTCCTCCAAGAGCACCTCTGGG 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GlyLysGlyLeuGluTrpIleGlyArglleTyrThrSerGlySerThrAsnTyrAsnPro
                                                                                                                                                                                                                                                                                                                                                                                                ATGAAACACTGTGGTTCTTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAG
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 ThrSerSerValAlaValGlyCysLeuAlaGlnAspPheLeuProAsp 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             475 ---GGCACAGCGGCCCTGGCTGGTCAAGGACTACTTCCCCGAA
                       Straubberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AAH11857.1; -.
InterPro; IPR003598; Ig_c2.
InterPro; IRR003006; Ig_MHC.
Pfam; PF00047; ig; 5.
SMART; SM00408; IGC2; 2.
PROSITE; EM00259; Ig_MHC; UNKNOWN_3.
Immunoglobulin domain.
SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;
                                                                                                                                                                                                                                               613
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNN-2002 (TrEMBLrel. 19, Last annotation update)
Hypothetical 53.4 kDa protein.
                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                          US-08-728-463B-219 (1-524) x Q96EY0 (1-613)
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641.00
78.41%
72.73%
66.29%
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Best Local Similarity:
FROM N.A.
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81 AsnProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 CCACCAGGTAAGGGTCTGGAGTGGATTGGTGAAATCAAAGTGGAAGCACCAACTAC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCGAGAGTA--- 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 ATTAATTGGTTCGACCCTTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCAACC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 LeuGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuSer 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 CysThrValSerGlyGlySerIleSerSerThrAsnTyrTyrTrpGlyTrpIleArgGln 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 AACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCT
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 51.8 kDa protein.
Hypothetical 51.8 kDa protein.
Hypothetical 51.8 kDa protein.
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Clonal proliferation of IgM secreting B cell in the synovium Behcet's patient with arthritis.";
Submitred (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF103795, AAC79084.1; --
HSSP, P01825; 7FAB.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; I.
                                                                                                                                                                                                                                 POTENTIAL.
VH4 HEAVY CHAIN VARIABLE REGION.
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Matches:
Conservative:
Mismatches:
Indels:
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583.50
84.21%
75.66%
60.34%
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TISSUE=SPLEEN;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity:
cal Similarity:
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150
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NON TER
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Query Match:
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21 LeuGlnLeuGlnGluSerGlyProGlyLeuValLysSerSerGluThrLeuSerLeuThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                       Strausberg R.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016369; AAH16369.1;
InterPro; IFPR03006; Ig_MHC.
Fram; PP00047; ig; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
WH4 heavy chain variable region precursor (Fragment)
IGM.
                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                            Hypothetical protein.
SEQUENCE 496 AA; 53391 MW; D346929849040D69
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SRQUENCE FROM N.A.
Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
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                                                                                                                                                                                                                                                                      2.49e-50
590.00
74.16%
67.42%
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SEQUENCE FROM N.A. TISSÜE=LUNG;
                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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us-08-728-463b-219.rspt

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InterPro; IPR003596; Ig_v.
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01-JUN 2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 17, Last sequence update)
11-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 52.0 kDa protein.
Hypothetical 52.0 kDa protein.
Buks musculus (Mouse).
Buks musculus (Mouse).
Mammalia; Metheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musi
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC024289; AAH24289.1; -. Hypothetical protein. SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Straubberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC002091; AAH02091.1; -.
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Matches:
Conservative:
Mismatches:
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InterPro; IPR003597; Ig c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
                                                                                                             8.8e-42
504.50
71.68%
60.12%
52.17%
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Best Local Similarity:
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                                                                                         Alignment Scores:
Pred. No.:
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140 AsnProThrileTyrFroLeuThr---LeuProProAlaLeuSerSerAspProVallle 158
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UL73;
01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
(Fragment).
Pfam; PF00047; 19, 4.
SMART; SM00409; 1G; 3.
SWART; SM00406; 1Gc1; 3.
SWART; SM00410; 1G like; 1.
PROSITE; PS00290; 1G MHC; UNKNOWN_2.
PROSITE; PS00290; 1G MHC; UNKNOWN_2.
SRQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
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23
43
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Matches:
Conservative:
Mismatches:
Indels:
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496.00
72.35%
58.82%
51.29%
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Best Local Similarity:
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|TrpGlyProTyrTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGG------TTCGACCCTTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 414
                                                                                                                                                                                                                                                               CAGGTGCAGCTACAGCAGTGGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTC
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                                                                                                                                                                                                                                                                                                                                                               CCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTCTG
                                                                                                                                                                                                                                                                           STRAIN-C57BL/6J; TISSUE-PANCREAS;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Baralov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
181006000Rik protein.
1GH-1 OR 1810060009Rik Muss musculus (Mouse).
Eukaryota; Metazoa; Ghordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
Young'D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;
                                                                                                                                                              119
95
7
13
4
                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                              Cin. Immunol. Immunopathol. 87:184-192(1998)

EMBL, AF035041; AAD56277.1; -.

HSSP; P01825; 7FAB.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.

Pfam; PF00047; ig; 1.
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                                                                                                                                                              1.4e-40
491.00
85.71%
79.83%
50.78%
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                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                     Alignment Scores:
                                                                                                                   NON_TER
SEQUENCE
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121 AspTyrAspTrpPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAlaAlaLys 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 GluLysPheLysGlyLysAlaThrLeuThrAlaAspLysSerSerThrAlaTyrMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 ---ATTAATTGGTTCGACCCTTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 GGTAAGGGTCTGGAGTGGATTGGTGAAATCAAT ---CATAGTGGAAGCACCAACTACAAC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 CCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTCTG 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 ValGlnLeuLysGlnSerGlyAlaGluLeuValLysProGlyAlaSerValLysIleSer
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Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                            161 ValThrLeuGlyCysLeuValLysGlyTyrPheProGluPro 174
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87
31
52
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Mismatches:
Indels:
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449.00
67.82%
50.00%
46.43%
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                                                                                                                                                                                                      Hayashizaki Y.;
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Pred. No.:
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Alignment Scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 GGTGAAATCAAT---CATAGTGGAAGCACCAACTACAACCGGTCTCTCAAGAGTCGAGTC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 ACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTCTGAAACTGAGGTCTGTGACCGCT 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379 CCTTGGGGCCAGGGAACCCTGGTCACCGTCTCAGCCTCAACCAAGGGCCCATCGGTC 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439 TICCCCCTGGACCCTCCAAGAGCACCTCTGGGGGCACAGGGGGCCCTGGGGTGCCTG 498
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28 AlaGluLeuValLysProGlyAlaSerValLysLeuSerCysLysAlaSerGlyTyrThr 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 LeuPheLeuValAlaThrAlaThrGlyValHisSerGlnValGlnLeuGlnGlnProGly 27
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48 PheThrSerTyrTrpMetHisTrpValLysGlnArgArgGlyGlnGlyLeuGluTrpIle 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 CTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCAGGTGCAGCTACAGCAGTGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 ValTrpGlyAlaGlyThrThrValThrValSerSerAlaLysThrThrAlaProSerVal
                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                    Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC012207, AAH12207.1; -.
InterPro; IRR003006; Ig_MHC.
Pfam; PP00047; ig; 2.
SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (protein for MGC:18977).
                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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|ValLysGlyTyrPheProGluPro 175
                          PRT;
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099L31;
01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                        1.55e-35
441.50
67.26%
52.38%
45.66%
                        PRELIMINARY;
                                                                                                                                           SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                                                  NCBI_TaxID=10090;
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Pred. No.:
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                     Q921K1
Q921K1;
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73 GIGCAGCIACAGCAGIGGGGGGGCAAGACTGTIGAAGCCTTCGGAGACCCTGTCCCTCACC 132
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| ThythralaProSerValTyrProLeualaProValCysGlyAspThrThrGlySerSer 160
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| MetLysCysSerTrpValIlePhePheLeuMetAlaValValIleGlyValAsnSerGlu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 CysThrAlaSerGlyPheAsnIleLysAspSerLeuMetHisTrpValLysGlnArgPro 60
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                                                                      Bukaryota, Metaoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butharia; Rodenia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                     Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC003878; AAH03878.1; --
HSSP; P01842; 7FAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96352328B3332ADB CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01.-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01.-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                 InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003509; IG_1:
InterPro; IPR003506; IG_1MHC.
InterPro; IPR003596; IG_V.
Pfam; PF00047; IG; 3.
SWART; SW00409; IG; 2.
SWART; SW00409; IG; 2.
SWART; SW00400; IG ILE; 1.
SWART; SW00410; IG ILE; 1.
SWART; SW00410; IG ILE; 1.
SRGUENCE 468 AA; 51661 MW; 9635232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.98e-33
421.00
63.22%
48.28%
                                                                                                                                                           SEQUENCE FROM N.A.
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Best Local Similarity:
Query Match:
DB:
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RESULT

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161 ValThrLeuGlyCysLeuValLys 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Targeting T cells to the CNS.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ416332; CAC94687.1; -..
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR001230; Prenyl_site.
SMART; SM00409; IG; I.
SMART; SM00406; IGv; I.
                                                                                                                                                                                                                                                                                                                                                                                                  Chernajovsky Y.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8VDC9;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Anti-MOG 212 variable gamma 2a (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                    PRT; · 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00294; PRENYLATION; UNKNOWN 1.
NON TER 168 168
SEQUENCE 168 AA; 18293 MW; 183719FCCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-728-463B-219 (1-524) x Q8VDC9 (1-168)
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420.00
64.29%
50.00%
                                                  PRELIMINARY;
                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=BALB/C;
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                             TRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
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Monoclonal antibody; immunoglobulin heavy chain; human
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Amino acid sequenc IgM antibody CEM 1

Amino acid sequenc Human TF anti-idio

F105 rearranged va Human 5' EST relat Human 5' EST relat Humanised 1D10 ant Humanised 1D10 ant

30-MAR-2000; 2000WO-JP02022

Database :

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Transformation of a hybridoma with a gene encoding an immunoglobulin
heavy chain polypeptide for enhanced production of monoclonal antibody
       99JP-0087929
                  (NISB ) JAPAN TOBACCO INC. (ABGE-) ABGENIX INC.
                                      Kusunoki C, Fukushima A;
                                                    WPI; 2000-611721/58.
                                                           N-PSDB; AAA09695
      30-MAR-1999;
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Example 2; Page 40-43; 48pp; Japanese.

This invention relates to a method for the production of a monoclonal antibody. The antibody is produced by inserting a gene encoding an immunoglobulin heavy chain polypeptide into cells which produce a monoclonal antibody recognizing the immunoglobulin, and culturing the transformant to express the antibody. The invention also includes transformant to expressing cells transformed by the method; and transgenic non-human animals containing the cells and expressing a human antibody. The method results in the enhanced expression of a monoclonal antibody for diagnostic and therapeutic use. The present sequence cobresents a human immunoglobulin heavy chain amino acid sequence, the containing the protein is used in an example of the method of the

Sequence 462 AA;

462 155 5 10 1 Length:
Matches:
Conservative:
Mismatches: 1.82e-65 812.00 93.02% 90.12% 83.97% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores:

US-08-728-463B-219 (1-524) x AAB26884 (1-462)

GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 132 GGTAAGGGTCTGGAGTGGATTGGTGAATCAATCATAGTGGAAGCACCAACTACAACCCG 252 312 CTGAGCTCTGTGACCGCTGCGGACACGCTGTGTTACTGTGCGAGA-----GTAATT 366 367 AATTGGTTCGACCCTTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCAACCAAG 426 72 9 80 TCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTCTGAAA ATGAAACACCTGTGGGTTCTTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCACA GGCCCATCGGTCTTCCCCCTGGCACCTTCCTCCAAGAGCACTCTGGGGGCACAGGGGCC 73 313 41 193 253 81 101 427 셤 ð ò 요 ò 원 ð 엄 ò 윱 g δ ò 셤 ò

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Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
CTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG 522
           SEQ ID NO:4331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; SEQ ID No 4331; 2922pp; English.
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                                                                     ABP43199 standard; Protein; 193
                                                                                                                                         Human ovarian antigen HVVDH44,
                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                      07-JUN-2001; 2001WO-US18569.
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                                                                                                                      (first entry)
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                                                                                             ABP43199;
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                                                         ABP43199
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABO\$4131-ABO\$5305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to encompasses polypeptides 90% identical and polynucleotides and host cells comprising human ovarian antigens. Of the sequences of the invention. The invention additionally relates to combinant vectors and host cells comprising human ovarian antigens, and the use comparation proprocedudes and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, clasorders (e.g., infertility, disorders of pregnancy, anovulation, clasorders (infertions e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and immunodificientories, autoimmune opphoritis, systemic lupus erythematosus), cspiratory disorders (e.g., anaemia), cardiovascular disorders (c.

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AAB36206;

RESULT g

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TGCGCTGTCTATGGTGGTTCCTTCAGT-----GGTTACTACTGGAGCTGGATCCGCCAG 186
                                                                                                                                                                                                                                                                                 CTGAAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCGAGAGTAATT 366
                                                                                                                                                                                                                                                                                                                                                         101 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgAspAsp 120
                                                                                                                                                                                                                                                                                                                                                                                                         ThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 179
                                        ------AATTGG---TTCGACCCTTGGGGCCAGGGAACCCTGGTCACC
                            ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAG
                                                                                    GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC
                                                                                                                                                                                                          GTCTCCTCAGCCTCAACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGC
                                                                                                                                                                                                                                                                   AACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCTCTGGGGGCACAGCGGCCCCTGGCCTGGTCAAGGACTACTTCCCCGAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic luque erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primatised anti-human B7.1 antigen antibody 16C10 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shestowsky WS;
US-08-728-463B-219 (1-524) x AAB36206 (1-473)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW01822 standard; Protein; 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric Macaca cynom
Chimeric Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-108638/10.
N-PSDB; AAT62513.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISAPs). These can be used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, arteriosclerosis, cirrhosis and cancer.
                            429
                                                                                       CCATCGGTCTTCCCCCTGGCACCCTCCTAAGAGCACCTCTGGGGGCACAGCGCCCTG 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human immune system associated proteins (HISAP) and polynucleotides
                                                                      TGGTTCGACCCTTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCAAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                      system associated protein; HISAP-4; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding the HISAP, useful for diagnosing, treating or preventing immune or cell proliferative disorders or infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baughn MR;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                       Human immune system associated protein HISAP-4.
              GACACGCTGTGTATTACTGTGCGAGAGTAATT-
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                                                                                                                                                                                                                                                                                                                                                                                                                       infection; autoimmune disease; cancer
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766.50
88.83%
86.03%
79.27%
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oung J;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                         immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Sequence

Query Match: DB:

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GCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACGCTGTCTATGGTGGTTCC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 GlyGluIleAenHisSerGlySerThrAenTyrAsnProSerLeuLysSerArgValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 ATATCAGTAGACACGTCCAAGAACCAGTTCTCTGAAAACTGAGCTCTGTGACCGCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in new-born rhesus positive babies. Recombinant IgM-D7C2 can be produced by insect cells which have been transformed by a baculoviral vector comprising a D7C2 expression cassette. The present sequence is that of a recombinant IgM-D7C2 heavy chain fused downstream of a mouse VH signal peptide.
                                                   20..472
/label= heavy_chain
/note= "human gamma 1 chain constant region
and the variable region from anti-rhesus
antibody D7C2"
                                     peptide sequence encoded
                                                                                                                                                                                                                                                                                                                       Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing
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1151
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Matches:
Conservative:
Mismatches:
Indels:
                       signal peptide
mouse VH signal po
synthetic linker"
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                                    /note= "mouse
                                                                                                                                                                                                                                                                                                                                               haemolysis in new-born babies
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(PROT-) PROTEINE PERFORMANCE.
                                                                                                                                                                            94FR-0010566
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783.00
89.47%
88.30%
80.97%
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/label=
                                                                                                                                                                                                                                                            Edelman L,
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N-PSDB; AAT26889.
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                           02-SEP-1994;
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                                                                                                                                                      08-MAR-1996,
                                                                                                                                                                                                                                                             Chaabihi H,
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           Peptide
                                                         Protein
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polypèptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                              GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGGCTTTCGGAGACCCTGTCCCTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human monoclonal antibody; immunoglobulin isotype IgM; agglutination; rhesus positive; rhesus negative; haemolysis; gamma 1 heavy chain; variable region; insect host cell; baculovirus; recombinant production.
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153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-rhesus D recombinant antibody D7C2 heavy chain.
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Matches:
Conservative:
Mismatches:
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85.47%
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Synthetic.
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(first entry)

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Macaque primatized 16C10 heavy chain protein.
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                                               2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and heavy variable genes (see also AATG2512 and AATG2513) are inserted into an expression vector (pref. NEOSPLA) which contains human light and antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1 antibodies have also been produced (see also AAW01877-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGGTAAGGGTCTGGAGTGGATTGGTGAAATC---AATCATAGTGGAAGCACCAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCGAGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------GTAATT------AATTGGTTCGACCCTTGGGCCAGGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCGTGCCTGGTCAAGGACTACTTCCCC
                                                                                                                                                                                                                                                                                                  ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAG
                                                                                                                                                                                                                                                                                                                                        GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCACC
                                                                                                                                                                                                                                                                                                                                                                                 TGCGCTGTCTATGGTGGTTCCTTCAGT----GGTTACTACTGGAGCTGGATCCGCCAGCCA
monoclonal antibody binding human B7.1 or B7.2 antigen for treating autoimmune disease or graft-versus-host di
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147
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                            US-08-728-463B-219 (1-524) x AAW01822
                               Claim 14; Fig 10B; 81pp; English
                                                                                                                                                     and graft-versus-host disease
                                                                                                                                                                                                     7.85e-59
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80.77%
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GluPro 182
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AAW63765 standard; Protein; 476 AA.

AAW63765 ID AAW6 XX

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This sequence represents a primatized form of the antibody 16C10 heavy chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigans and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving a really interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpure, systemic lupus erythematosus, type inflammatory bowel disease, allergy and multiple sclerosis, graft vs. Corn filammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the Mab can be conjugated to a drug or toxin. MAb's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAb's are optionally combined with other proteins induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppression, i.e. it inhibits antigen-specific immunosuppression, i.e. it inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fonoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80; DD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B
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739.00
85.16%
80.77%
76.42%
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                                                                                                                     cell proliferation.
                                                                                                                                                                                 Macaca fascicularis.
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         Monoclonal
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8; Fig 5b; 89pp; English.

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Protein sequence of primatised form of the heavy chain of 16C10 antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                          AAU11646 standard; Protein; 476 AA
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                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Homo sapiens.
Chimeric - Macaca sp.
Synthetic.
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Length:
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Mismatches:

7.85e-59 739.00 85.16% 80.77% 76.42%

476 AA;

Indels: Gaps:

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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as idiopathic thrombocytopenia purpura, systemic lique, erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-ves-host disease. The antibody is useful for immunosuppression or graft-ves-host disease. The antibody is useful for immunosuppression or graft-ves-host disease. The antibody is useful for immunosuppression or ejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive and hyperproliferative collitis, food-related allergies e.g. migrain, rhinitis and eczema, and other types of allergies. The present protein sequence represents the heavy chain of 16C10, a primatised antibody cused in the invention to induce apoptosis and inhibit production of interleukin-2 (IL-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
                                        TGCGCTGTCTATGGTGCTTCCTTCAGT---GGTTACTACTGGAGCTGGATCCGCCAGCCA
                                                                                                                                                                                                                                    CTGAAACTGAGGTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCGAGA-----
                                                                     CCAGGTAAGGGTCTGGAGTGGATTGGTGAAATC---AATCATAGTGGAAGCACCAACTAC
                                                                                                                                                   AACCCGTCTCAAGAGTCGAGTCACCATATCAGTAGACGGTCCAAGAACCAGTTCTCT
                                                                                                                                                                                                                                                                                                                                                                                   -----GTAATT------AATTGGTTCGACCCTTGGGGCCAGGGAACC
21
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132 TGCGCTGTCTATGGTGGTTCCTTCAGT - - GGTTACTACTGGAGCTGGATCCGCCAGCCA 189 CCAGGTAAGGGTCTGGAGTGGATTGGTGAAATC---AATCATAGTGGAAGCACCAACTAC 246 306 CTGAAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCGAGA---- 360 -----GTAATT-----AATTGGTTCGACCCTTGGGCCAGGGAACC 396 456 160 40 72 61 ProGlyLysGlyLeuGluTrplleGlySerPheTyrSerSerSerGlyAsnThrTyrTyr 80 GTGCAGCTACAGCAGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 13 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCAG AACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCT CTGGTCACCGTCTCCTCAGCCTCAACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCTCAGGACTACTTCCCC US-08-728-463B-219 (1-524) x AAU11646 (1-476) 133 73 190 247 81 307 457 101 361 121 397 g ò ò g ò g ò . Q ò 셤 ò g g ò ò ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -useful for treating autoimmune disease or graft-versus-host disease
                                                                                                                                                                                                        Monoclonal antibody; cynomolgus monkey; macaque; 7C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid archritis; psoriasis; type I diabetes mellitus; graft versus host disease;
          161 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 176
                                                                                                                                                                            Primatised anti-human B7.1 antigen antibody 7C10 heavy chain.
GGCACAGCGCCCTGGCCTGCCTGGTCAAGGACTACTTCCCCGAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shestowsky WS;
                                                                                      AAW01818 standard; Protein; 476 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Fig 8B; 81pp; English.
                                                                                                                                                                                                                                                                                    hetero-hybridoma; transfectoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and graft-versus-host disease
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                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US10053
                                                                                                                                                                                                                                                                                                                  Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IDEC-) IDEC PHARM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                           247 AACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCT 306
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                                                                                                                TGCGCTGTCTATGGTGGTTCCTTCAGTGGT - - TACTACTGGAGCTGGATCCGCCAGCCA
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21 VallysLeuGlnGlnTrpGlyGlvGlyLeuLeuGlnProSerGluThrLeuSerAgThr
                                                                                                                                                                                                                                                           CCAGGTAAGGGTCTGGAGTGGATTGGTGAATCAATCATAGTGGA---AGCACCAACTAC
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13 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAG

US-08-728-463B-219 (1-524) x AAW01818 (1-476)

8 8

476 143 7 20 12 3

Length:
Matches:
Conservative:
Mismatches:
Indels:

2.75e-57 722.00 82.42% 78.57%

Similarity:

Query Match: DB:

Percent Similarity:

Immune system molecules used in the diagnosis, treatment and prevention of disorders associated with the immune system and cell proliferation

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Patterson

Guegler KJ,

Gorgone G,

Corley NC,

Tang YT,

(INCY-) INCYTE PHARM INC

99WO-US13995 98US-0107223

21-JUN-1999; 30-JUN-1998;

06-JAN-2000

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WPI; 2000-170916/15.
N-PSDB; AAZ50012.
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Baughn MR;
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                                                                                                                              Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis; treatment; prevention; cell proliferation; immune system disorder.
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/note= "shows similarity to Ig superfamily protein
domain"
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/note= "shows similarity to Ig superfamily protein
domain"
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/note= "conserved Ig/MHC protein block"
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|Tabel= Signal_peptide
|20..470
|Tabel= Mature_ISMO-2
                                                                                                          Human immune system molecule, ISMO-2,
                                                                                                                                                                                 location/Qualifiers
                                               AAY44721 standard; Protein; 470 AA.
                                                                                        (first entry)
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GluPro 182
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GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 132
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                               The present sequence is an immune system molecule, ISMO-2 from an Incyte clone 2849752 isolated from the human breast tumour CDNA library (BRSTTUT13). This sequence is expressed in several libraries, generally those associated with cancer, cell proliferation, immune response or trauma. It shows homology to vertebrate immunoglobulin gamma heavy-chain. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with the immune system and cell proliferation.
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Matches:
Conservative:
Mismatches:
Indels:
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Claim 1; Pages 60-61; 69pp; English.
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729.00
85.23%
81.82%
75.39%
                                                                                                                                                                                                     470 AA;
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Best Local Similarity:
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WO200000608-A2.

AAU11539 standard; Protein; 476 AA

(first entry)

12-MAR-2002

AAU11539;

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AAU11539
                                                 This sequence represents a primatized form of the antibody 7C10 heavy chair from macaque. This sequence is used in a method which studies new monoclonal antibodies (MAb's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibite binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAb's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppression, i.e. it inhibits antigen-specific immunosuppression, i.e. it inhibits antigen-specific immunosuppression.
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143
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Matches:
Conservative:
Mismatches:
Indels:
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           Example 7; Fig 3b; 87pp; English
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74.66$
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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ calls. The invention is.

(CD86) for inducing the apoptosis of B7+ calls. The invention is.

(CD86) for inducing the apoptosis of B7- calls. The invention is.

(CD86) for inducing the seases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell lenkaemia, and autoimmune diseases such as B cell inducer, in a call inflammatory bile disease, allergy, multiple calcarosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. migraine, rhintis and eczema, and other types of allergies. The present protein sequence represents the heavy chain of 7010, a primatised antibody used in the invention to induce apoptosis and inhibit production of
                                                               Human; macaque monkey; light chain; primatised antibody; 7C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leuksemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection;
Protein sequence of primatised form of the heavy chain of 7C10 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such a
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Chimeric - Macaca sp.
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                                                                                                                                                         CTGAAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTATTACTGTGCGAGA-
                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.
                 CCTCCTGGTGGCAGCTCCTAGATGGGT
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/note= "Mature heavy chain"
US-08-728-463B-219 (1-524) x AAU11539 (1-476)
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/note= "Signal peptide"
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               ATGAAACACCTGTGGTTCTTCCT
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65 kD antigen;
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                                             Human monoclonal antibody binds to cytomegalovirus 65 kD antigen produced by primer amplification, used in the disgnosis of hCMV
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Matches:
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Mismatches:
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                                                                                                  Claim 4; Page 16-18; 22pp; Japanese.
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ID AAY96290 standard, protein, 537
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80.11%
73.89%
WPI; 1996-154852/16.
N-PSDB; AAT18059.
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Best Local Similarity:
Query Match:
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us-08-728-463b-219.rag

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders
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                                                                 Human; immunoglobulin; IGFAM-2; IGFAM; immune disorder; cancer;
infection; inflammation; haematopoiesis; AIDS; allergy.
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Yang J;
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/label= signal_peptide
27..537
/label= IGFAM-2
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/label= Ig_signature
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/label= Ig_signature
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/label= Ig_domain
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/label= Ig_domain
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98US-0113635.
99US-0128194.
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Lal P, Hillman JL,
                                            Human IGFAM-2 immunoglobulin
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                     16-AUG-2000 (first entry)
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07-APR-1999;
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                                                                                                                                                  8 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpValLeuSerGln
                                                                                                                                                                                                                                                                                                                                                                                          457 TCCAAGAGCACCTCTGGGGGCACA---GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC
                                                                                                                                 13 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAG
                                                                                                                                                                                          73 GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC
                                                                                                                                                                                                           28 ValGinLeuGinGinTrpGlyAlaGlyLeuLeuLysProSerGiuThrLeuSerLeuThr
                                                                                                                                                                                                                                                                    68 IleArgGlnProProGlyLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySer
                                                                                                                                                                                                                                                                                                                                                                       238 ACCAACTACAACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGITCICICIGAAACIGAGCICIGIGACCGCIGGGACACGGCIGIGIATIACIGIGGG
                                                                                                                                                                                                                                                                                                              monoclonal antibody; chimaeric antibody; recombinant antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cynomolgus monkey, autoîmmune disease; rheumatoid arthritis;
leukaemia; lymphoma; graft-versus-host disease; asthma;
transplant rejection; HIV; therapy; CE9 gamma 4PE.
537
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            Matches:
Conservative:
Mismatches:
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                                                       Indels:
Length:
                                                                                                    US-08-728-463B-219 (1-524) x AAY96290 (1-537)
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            706.50
80.11%
77.35%
73.06%
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                                            Similarity:
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Misc-difference
                           Percent Similarity:
Best Local Similari
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                                                       Query Match:
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AAW14927
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GCCTCAACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGG 474
                                                                                              ---AGAGTAATTAATTGGTTCGACCCTTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
                                                                                                                                                                                                                                                                                                                                         CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; cynomolgus monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CE9 gamma 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 Polypeptides (AAW14925-27) respectively comprise the heavy chain regions of human gamma-4, gamma-4E carrying an L236E mutation in the hinge region, and gamma-4PE carrying L236E and 8229P mutations. They can be incorporated into novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human Ig64 Fc binding domain framework is complianed with the antigen binding domains (see also AAW14922-23) of macaque antibuman CD4 monoclonal antibody E9.1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. They can be used to treat autoimmune diseases such as rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4 mediated immune functions, espuseful for treatment of autoimmune disease, e.g. rheumatoid arthritis
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Mismatches:
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Gaps:
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                                                                                                                                                                                                                          AAW14925 standard; Protein; 467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reff ME;
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700.00
84.66%
78.98%
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                                                                                                                                                                                                                                                                                                               Human gamma-4 heavy chain.
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Query Match;
DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT62868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGGTAAGGGTCTGGAGTGGATTGGTGAATCAATCATAGT---GGAAGCACCAACTAC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ProGlyLysGlyLeuGluTrp11eGlyTyr11eTyrGlySerGlyGlyGlyThrAsnTyr 80
                                                                                                                                                                                                                                                                                                                                              1 Polypeptides (AAW14925-27) respectively comprise the heavy chain regions of human gamma-4, gamma-4E carrying an L236E mutation in the hinge region, and gamma-4PE carrying L236E and S229P mutations. They can be incorporated into novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human 1gG4 FC binding domain framework is combined with the antigen binding domains (see also AAW1492-23) of macaque antibuman CD4 monoclonal antibody E9.1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. The gamma-4E and cape mutations confer activity enhanced stability and eliminate depleting activity. The antibodies can be used to treat autoimmune diseases such as rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCAG
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                                                                                                                                                                                                                                              Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, espuseful for treatment of autoimmune disease, e.g. rheumatoid arthritis
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 /note= "Bite of L236E mutation"
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Best Local Similarity:
Query Match:
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                            WO9709351-A1
                                                                                   05-SEP-1996;
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Pred. No.:
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73 GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 132
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                                                                                                                                                   CCAGGTAAGGGTCTGGAGTGGATTGGTGAAATCAAAGT---GGAAGCACCAACTAC 246
                                                                                                                                                                                                                                                                                           AACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACCACGTCCAAGAACCAGTTCTCT 306
                                                                                                                                                                                                                                                                              ---AGAGTAATTAATTGGTTCGACCCTTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 414
                                                                                                                                                                                                                                                                                                                      415 GCCTCAACCAAGGGCCCATCGGTCTTCCCCTGGCACCTTCCAAGAGCACCTCTGGG 474
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Search completed: June 3, 2003, 09:02:28 Job time: 39:0597 secs

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Sequence 12, Application US/10124905

Sequence 12, Application US/10124905

Patent NO. US20020166136A1

Fatent NO. US20020166136A1

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                    Sequence 93, Appl Sequence 1642, Appl Sequence 1642, Appl Sequence 1642, Appl Sequence 25, Appl Sequence 25, Appl Sequence 113, Appl Sequence 113, Appl Sequence 113, Appl Sequence 125, Appl Sequence 126, Appl Sequence 126, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 113, Appl Sequence 1413, Appl Sequence 1413, Appl Sequence 1413, Appl Sequence 15, Appl Sequence 17, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25
                                Sequence 10, Appl
Sequence 110, Appl
Sequence 110, App
Sequence 145, App
Sequence 37, Appl
Sequence 21, Appl
Sequence 21, Appl
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Sequence 2, Appli
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Sequence 44315,
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Sequence 218, 1
Sequence 250, 7
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Sequence 218,
Sequence 250,
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US-10-211-357-8
US-10-211-357-10
US-10-211-357-10
US-10-211-357-10
US-10-211-357-10
US-10-194-975-110
US-09-880-748-1321
US-09-910-059-93
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US-09-990-288-218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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FILING DATE:
CLASSIFICATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
      \begin{array}{c} \mathbf{744408141} \\ \mathbf{74408141} \\ \mathbf{7000080471} \\ \mathbf{7000080471} \\ \mathbf{7000080471} \\ \mathbf{7000080471} \\ \mathbf{7000080471} \\ \mathbf{7000080471} \\ \mathbf{7000080471} \\ \mathbf{7000080471} \\ \mathbf{7000080471} \\ \mathbf{7000080471} \\ \mathbf{7000080471} \\ \mathbf{700080471}                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Command line parameters:
-MODEL=frame+ n2p.model -DBV=xlp
-MODEL=frame+ n2p.model -DBV=xlp
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-Q=/CG02 1/USPTO_Bpool/US0872B463/runat 03062003_085618_16959/app_query.fasta_1.3690
-DB=Published Applications AA -QFWT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bit 8 -START=1 -END=-1 -MATRIX=blosum62
-TRAMS=human40.cdi -LIST=45 -DOCALIGN=200 -THR MAXE=10
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-FGAPENT=7 -YGAPED=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 12, Appl
Sequence 4, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                       (without alignments)
4764.744 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                              1 AAGCTTGCCACCATGAAACA......GACTACTTCCCCGAACCGGT 524
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1: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
                                                                     Compugen Ltd
                                                                                                                                                                 protein search, using frame_plus_n2p model
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US-09-948-429B-12
US-10-124-905-4
US-09-948-429B-4
                                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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967
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seq length: 200000000
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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMINOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCGCTGTCTATGGTGGTTCCTTCAGT -- - GGTTACTACTGGAGCTGGATCCGCCAGCCA 189
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1147
115
124
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-728-463B-219 (1-524) x US-09-948-429B-12 (1-476)
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Matches:
Conservative:
Mismatches:
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APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN. Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
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739.00
85.16%
80.77%
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APPLICATION NUMBER: US
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-09-948-429B-12
                                                                                                                                                                        CITY: Alexandria
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Best Local Similarity:
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CLASSIFICATION:
                                                                                                                                                                                                           USA
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Mismatches:
Indels:
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Matches:
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       FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTATION UNMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEFRAN: 703-836-2021
TELEFRAN: 703-836-2021
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US-09-948-429B-12
; Sequence 12, Application US/09948429B
; Patent No. US20020177689A1
 09/383,916
                                                                                                                                                             TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                     739.00
85.16%
80.77%
76.42%
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MOLECULE TYPE: protein
APPLICATION NUMBER:
                                                                                                                                                                                                                                       amino acid
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Best Local Similarity:
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Sequence 4, Application US/09948429B
Patent No. US20020177689A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF FITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGAAACTGAGCTCTGTGACCGCTGCGGACACGCTGTGTATTACTGTGCGAGA---- 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GTAATTAATTGGTTCGACCCTTGGGGCCAGGGAACC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ArgProAspCysThrThrIleCysTyrGlyGlyTrpValAspValTrpGlyProGlyAsp 140
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                                                                                               21 ValLysLeuGlnGlnTrpGlyGluGlyLeuLeuGlnProSerGluThrLeuSerArgThr 40
                                                                                                                                                                                                                                        GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
                                          US-08-728-463B-219 (1-524) x US-10-124-905-4 (1-476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, V. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
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181 GluPro 182
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US-09-948-429B-4.
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                           ||||-::
| LeuPheSerValValGlyMetValTyrAsnAsnTrpPheAspValTrpGlyProGlyVal 140
                                                                                                                                              456
                                                                                                                                                             516
                                                                                                                                                                                                                                    SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro 180
------GTAATT-------AATTGGTTCGACCCTTGGGGCCAGGGAACC
                                                                                                                                                                                                                TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGCTGCTGGTCAAGGACTACTTCCCC
                                                                                                                                            CTGGTCACCGTCTCCTCAGCCTCAACCAAGGGCCCCATCGGTCTTCCCCCTGGCACCTCC
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143
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,905
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Mismatches:
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Matches:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PPLICATION NUMBER: 09/383,916
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
ATTORNEY AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 4, Application US/10124905; Patent No. US20020166136A1; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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82.42%
78.57%
74.66%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
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|81 GluPro 182
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Best Local Similarity:
Query Match:
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US-10-124-905-4
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                                 Nowman, Roland A.
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies
Therapy
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110
21
6
3
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ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: «UNKNOWN»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) TOPOLOGY: linear ;
MOLECULE TYPE: protein ;
SEQUENCE DESCRIPTION: SEQ ID NO: 8: US-10-211-357-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSERS: BURNS, DOANE, STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELEFAX: 703-836-202
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700.00
84.66$
78.98$
                 APPLICANT: Hanna, Nabil
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                                                                                                     NUMBER OF SEQUENCES:
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Best Local Similarity:
Query Match:
DB:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATORNEX/AGENT INFORMATION:
RAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-2021
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; Publication No. US20030077275A1
; GENERAL INFORMATION:
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82.42%
78.57%
74.66%
                                                                                                                                                             TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity:
Query Match:
DB:
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                                                                 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln
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                                                                                                                                                                                                                                                                                                                                                                                                                   61 ProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrGlySerGlyGlyGlyThrAsnTyr
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                                      ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 AACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCT
                                                                                                                                                                                    21 ValGlnLeuGlnGluSerGlyProGlyLeuValLy8ProSerGluThrLeuSerLeuThr
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Reff, Mitchell B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 SerThrAlaAlaLeuGlyCysLeuVallysAspTyrPheProGluPro 176
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
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APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523,894
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REPLICATION NUMBER: US/10/211,357
FILING DATE: 05-AUG-2002
CLASSIFICATION: «Unknown»
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ADDRESSERS BURNS, DOANE, STREET: 699 Prince Street
CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-211-357-12; Sequence 12, Application US/10211357; Publication No. US20030077275A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hanna, Nabil
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COUNTRY: USA
ZIP: 22314-3187
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LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaSerAsnIle 120
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                                                                                                                                                             Newman, Roland A.
Reff, Mitchell B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human Therapy
                                                                                                                         ---AGAGTAATTAATTGGTTCGACCCTTGGGGCCAGGGAACCCTGGTCACCGTCT
                                                                                                                                                                                                                                                                                                                                                                                     161 SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 176
                                                                                                                                                                                                                                                                                                                                                  475 GGCACAGCGGCCCTGGGCTGCTGAAGACTACTTCCCCGAACCG 522
           CTGAAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCG
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MEDIUM TYPE: Ploppy disk
COMPUTER: IN PC compatible
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIETCATION: <unimode color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the
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Mismatches:
Indels:
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
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Matches:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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ADDRESSEE: BURNS, DOANE, STREET: 699 Prince Street CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/10211357
Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity:
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Pred. No.:
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DB:
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124 TCCCTCACCTGCGCTGTCTATGGTGGTTCCTTCAGTGGTTACTACTGGAGCTGGATCCGC 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 SerLeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlu 121
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9 LeuAlaSerMet-------PheValPheSerIleAlaThrAsnAlaTyr---
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1133
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                                                       FEATURE:
OTHER INFORMATION: humanized chimeric D1.3 antibody
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Matches:
Conservative:
Mismatches:
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Patent No. US20020068319A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: PZ044P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/800,729 CURRENT FILING DATE: 2001-03-08
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PRIOR PILING DATE: 2000-09-22
PRIOR PILING DATE: 1099-09-24
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 145
                      TYPE: PRT
ORGANISM: Artificial sequence
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638.00
83,33%
76,44%
65.98%
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ORGANISM: Homo sapiens
                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                           US-10-194-975-110
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US-09-800-729-145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrGlySerGlyGlyGlyThrAsnTyr
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Matches:
Conservative:
Mismatches:
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Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: FOOLE, Jefferson
TITLE OP INVENTION: Super Humanized Antibodies
FILE REFERRACE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 110
                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                             Gaps:
TELECOMMUNICATION INFORMATION
                   TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                     LENGTH: 467 amino acids
TYPE: amino acid
                                                 INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS
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Best Local Similarity:
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US-10-194-975-110
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Sequence 1321, Application US/0980748

Publication No. US2003005937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 00/212,210

PRIOR PILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

SOFTWARE: PRIOR PRIOR IN NUMBER: 60/277,379

NUMBER: OF SEQ ID NOS: 3239

SOFTWARE: PARCELING DATE: 2001-03-25

NUMBER: OF SEQ ID NOS: 3239

SOFTWARE: PARCELING DATE: 2001-03-25

LENGTH: 249
                                                                    229
124
9
18
11
                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                     609.50
82.10%
76.54%
63.03%
; ORGANISM: Homo sapiens
US-09-974-449-37
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GluPro 162
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                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-880-748-1321
                                                    Alignment Scores:
Pred. No.:
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is Sequence 37, Application US/0997449

is Patent No. US20020141989A1

is GENERAL INFORMATION:

is APPLICANT: Kricek, Franz

shapticant: Vogel, Monique

is APPLICANT: Vogel, Monique

is TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODIES AGAINST

TITLE OF INVENTION: ANTI-DIOTYPIC ANTIBODIES AGAINST

TITLE OF INVENTION: ANTIBODIES WHICH INHIBIT THE BINDING OF IMMUNOGLOBULIN E TO

TITLE OF INVENTION: ANTIBODIES WHICH INHIBIT THE BINDING OF IMMUNOGLOBULIN E TO

TITLE OF INVENTION: ANTIBODIES WHICH AFFINITY RECEPTOR

TITLE OF INVENTION: ANTIBODIES WHICH AFFINITY RECEPTOR

TITLE OF INVENTION: ANTIBODIES WHICH AFFINITY RECEPTOR

TITLE OF INVENTION: ANTIBODIES WHICH AFFINITY RECEPTOR

TITLE OF INVENTION NUMBER: DS/09/974,449

CURRENT APPLICATION NUMBER: PSC/CEPOO/0328B

PRIOR FILING DATE: 2001-04-12

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 37

TYPE: PRI
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-974-449-37
                                     Alignment Scores
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Sequence 68, Application US/09187693

Sequence 68, Application US/09187693

Sequence 10. US20020173629A1

SENERAL INFORMATION:

APPLICANT: Sando, Michael

APPLICANT: Gallo, Michael

APPLICANT: Jia, Xiao-Chi

TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal

TITLE OF INVENTION: Human Monoclonal Antibodies to UNRENT FILING DATE: 1998-11-05

CURRENT FILING DATE: 1998-11-05

PRIOR APPLICATION NUMBER: US/09/22

PRIOR APPLICATION NUMBER: 09/162,280

PRIOR APPLICATION NUMBER: 09/162,280

PRIOR APPLICATION NUMBER: 09/162,280

PRIOR PILING DATE: 1997-05-05

NUMBER OF SEQ ID NOS: 75

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 152
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Matches:
Conservative:
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OTHER INFORMATION: Xaa = Any Amino Acid
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ORGANISM: human
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| Publication No. US20030086930A1
| GENERAL INFORMATION:
| APPLICANT: PRIZER PRODUCTS INC.
| TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
| FILE REFERENCE: PC23019A
| CURRENT APPLICATION NUMBER: US/10/153,382
| CURRENT FILING DATE: 2002-05-22
| PRIOR APPLICATION NUMBER: 60/293042
| RIGHT OF TILING DATE: 2001-05-23
| NUMBER: OF SEQ ID NOS: 39
| SOFTWARE: PatentIn Ver. 2.1
| SEQ ID NO 2: 1
| LENGTH: 172
| TYPE: PRI | TYPE: TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: PRI | TYPE: 
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Matches:
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Matches:
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71.75%
68.36%
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585.50
                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1321
                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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Pred. No.:
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Score:
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Query Match:
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Best Local Similarity: 65.90% Mismatches: 37 Query Match: 57.91% Indels: 6 DB: 3	US-08-728-463B-219 (1-524) x US-09-910-059-93 (1-260)	Qy 22 CTGTGGTTCTTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAGGTGCAG 78	Oy 79 CTACAGCAGTGGGGGGGCTGTTGAAGCCTTCGGAGACCCTGTCCCTGCGCT 138	Qy 139 GTCTATGGTGCTTCAGTGGTTACTAGAGCTGGATCGGCCAGCCA	Qy 199 GGTCTGGAGTGGATTGGTGAATCAATCATAGTGGAAGCACCAACTACAACCCGTCT 255	Qy 256 CTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTGTGAAACTG 315 ::	Qy 316 AGCTCTGTGCGCTGCGGACACGGCTGTGTATTACTGTGCGAGAGTAATTAAT	Oy 370TGGTTCGACCCTTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCAACC 423	Qy 424 AAGGGCCATCGGTCTTCCCCTGGCACCTCCTCCAGAGCACTCTGGGGGCACAGCG 483	Qy . 484 GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG 522 	RESULT 15 US-09-880-748-957 US-09-880-748-957 Sequence 957, Application US/0980748 Publication No. US2003059937A1 GENERAL INFORMATION: APPLICANT RUben et al. TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS TITLE REFERENCE: PF5.3 CURRENT FILING DATE: 2001-06-15 PRIOR PELICATION NUMBER: 60/210,210 PRIOR PELICATION NUMBER: 60/240,816 PRIOR PLICATION NUMBER: 60/277,379 PRIOR PLING DATE: 2001-03-16 PRIOR PLING DATE: 2001-03-21 PRIOR PLING DATE: 2001-03-21 PRIOR PLING DATE: 201-03-21 PRIOR PLING DATE: 201-05-25 NUMBER OF SEQ ID NOS: 3239 SOFTWARE: PRT CORGANISM: HOMO Sapiens US-09-880-748-957 Alignment Scores: 113 Score: 559.00 Matches: 113	
Best Local Similarity: 80.82% Mismatches: 20 Query Match: 59.05% Indels: 7 DB: 9 Gaps: 1	US-08-728-463B-219 (1-524) x US-09-187-693-68 (1-152)	Oy 106 AAGCCTTCGGAGACCCTGTCCTCACCTGCGCTGTCTATGGTCGTTCCTTCAGTGGTTAC 165	Oy 166 TACTGGAGCTGGATCCGCCACCACCAGGTAAGGGTCTGGAGTGGATTGGTGAAATCAAT 225	Oy 226 CATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGAC 285 :::	Oy 286 ACGTCCAAGAACCAGTTCTCTGAAACTGAGCTCTGTGAGCGCTGCGGGACACGGCTGTG 345	Oy 346 TATTACTGTGCGAGAGTAATTAATTGGTTCGACCCTTGGGGC 387	Oy 388 CAGGGAACCCTGGTCACCGTCTCCTCAGCCTCAACCAAGGGCCCATCGGTCTTCCCCCTG 447	Oy 448 GCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT-GGTCAAGGA 506	Oy 507 CTACTTCCCGAACGGT 524	RESULT 14 US-09-910-059-93 ; Sequence 93, Application US/09910059 ; Parent No Insononiasean	GENERAL INFORMATION APPLICANT: CORJOURING APPLICANT: CORJOURING APPLICANT: CORJOURING APPLICANT: Emery, Stephen Charles TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody, TITLE OF INVENTION: Their Therapeutic use in an Adept System TITLE OF INVENTION: Their Therapeutic use in an Adept System TITLE OF INVENTION: Their Therapeutic use in an Adept System TITLE OF INVENTION: Their Therapeutic use in an Adept System TITLE OF INVENTION: Their Therapeutic use in an Adept System TITLE OF INVENTION: THEIR TOWNER: US/09/910,059 CURRENT APPLICATION NUMBER: US/09/11,945 FRIOR FILING DATE: 1998-10-29 FRIOR FILING DATE: 1999-10-29 FRIOR PRILING DATE: 1999-02-14 FRIOR APPLICATION NUMBER: GES609405.7 FRIOR APPLICATION NUMBER: GES609405.7 FRIOR FILING DATE: 1996-05-04 FRIOR FILING DATE:	

	Percent Si	Similarity:	74.078		7	
á	Query Mat DB:		57.81% 9	Mismatches: Indels: Gaps:	222 2022	
7. 1	US-08-728	-728-463B-219 (1-	(1-524) x US-09-880-748-957	-748-957 (1-249)		
	È	70 CAGGTGCA	CAGGIGCAGCTACAGCAGGGGGGGGACTGTTGAAGCCTTCGGAGACCTG	SCAGGACTGTTGAAGC	тссстс	129
	qq	1 GlnValGl				20
	ò	130 ACCTGCGC	TGTCTATGGTGGTTCCT	rcagreerracracr	ACCTGCGCTGTCTATGGTGGTTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCA	189
	ΩÞ	21 ThrCysAla		 heSerAsnTyrTyrTı		40
	.0y	190 CCAGGTAAC	GGTCTGGAGTGGATTG	GTGAAATCAATCATA	CCAGGTAAGGGTCTGGAGTGGATTGGTGAATCATAGTGGAAGCACCAACTACAAC	249
	Ωp	41 ProGlyLys				09
	ò	250 CCGTCTCT	CAAGAGTCGAGTCACCA	TATCAGTAGACACGT	CCGTCTCTCAAGAGTCGAGCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTCTG 3	309
	ДD	61 ProSerLev				. 80
	ò	310 AAACTGAGG	CTCTGTGACCGCTGCGG	ACACGGCTGTGTATT	AAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCGAGAGTAATTAAT	369
	Dþ		Thral			100
	à	370 TGGTTC		B	GACCCTTGGGGCCAGGGAACC 3	396
	QQ	101 TyrTyrAsp	olleLeuThrGlyTyrT	 yrProSerGlyMetAe		120
	ò	397 CTGGTCACC	CTGGTCACCGTCTCCTCA		GCCTCAACCAAGGGC 4	429
	qa	121 LeuValThr		lyGlySerGlyGlyGl	 LeuValThrValSerSerGlyGlyGlyGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlyGly	140
	δ	430 CCATCGGTC	TTCCCCCTGGCACCCT	CCTCCAAGAGCACCTC	CCAȚÇGGICTICCCCCTGGCAÇCTCCTCCAAGAGCACCTGGGGGGACAGCGGCCCTG 4	. 489
	gg	 SerSerGlu	: TeuThrGlnAspProA	:: laValSerValAlaLe	 	160
	ò	490 GGCTGC 495	5			
	Db	161 ThrCys 162				÷

Search completed: June 3, 2003, 09:51:24 Job time: 26.264 secs

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93, Appl
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APPLICANT: EDELMAN, LENA
APPLICANT: EDELMAN, LENA
APPLICANT: CHABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEE: P.C.
F: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
CONFUTER: IBM PC COMPATIBLE
CONFORME: PATENTIN FORM: BC COMPATIBLE
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: O2-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
US-08-397-411-6
US-08-397-411-7
US-09-311-945-93
US-09-109-2070-20
US-09-109-2070-20
US-09-109-2070-20
US-08-887-352B-25
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    USA
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-LOOPEXT=0_-UNITS=bits -START=1 -END=-1_-MATRIX=blosum62_-TRANS=human40.cdi
-LIST=45_-DOCALIGN=200 -THR_SCORE=pct -THR_MX=100 -THR_MIN=0_-ALIGN=15
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-FGAPEXT=7_-YGAPPOP=10_-YGAPEXT=0.5_-DELOPE6_-DELEXT=7_-
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Sequence 12, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 118, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                        3, 2003, 09:02:35 ; Search time 11.9272 Seconds (without alignments) 2585.294 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-049-672A-4
US-08-487-550-12
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US-08-523-894-12
US-08-630-820-7
US-08-630-820-7
US-08-630-84-37
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US-08-793-450-4
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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US-09-049-672A-4
                         STREET: 3174 Por
CITY: Palo Alto
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                     34 CTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAGGTGCAGCTACAGCAGGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Yea, Y. Tom
APPLICANT: Yea, Henry
APPLICANT: Wea' Voung, Janice
APPLICANT: Gorley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
CORRESPONDENCE: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 GACACGCTGTGTATTACTGTGCGAGAGTAATT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09049672A; Patent No. 6135941; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTER.GTICS:
TYRE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-793-450-8
                                                                                                                                               6.2e-69
780.00
89.47%
87.72%
80.66%
                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                     Alignment Scores:
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73 GTGCAGCTACAGCAGGAGGCGCAGGACTGTTGAAGGCTTTCGGAGACCCTGTCCCTCACC 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 AACCGTCTCTCAAGAGTCGAGTCACATATCAGTAGACACGTCCAAGAACCAGTTCTCT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 AsnProSerLeuLygSerArgValThrIleSerValAspThrSerLygAsnGlnPheSer 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ProProGlyLysGlyLeuGluTrpileGlyTyrileTyrTyrSerGlySerThrLeuTyr 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 CCACCAGGTAAGGGTCTGGAGTTGGTGAAATCAATCATAGTGGAAGCACCAACTAC
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                                                                                                                                                                 COMPUTER: LEM COMPACIONE

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A

FILING DATE: HEREWITH
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTOMACA APPLICATION NUMBER:
REJENTENTY/AGENT INFORMATION:
NAME: CEATONE, Michael C
REGISTRATION NUMBER: 39,332

REFERENCE/DOCKET NUMBER: PP-0497 US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555

TELEPHONE: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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Incyte Pharmaceuticals, Inc.
4 Porter Drive
                                                STATE: CA
COUNTRY: USA
ZIP: 9430A
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.33e-67
766.50
88.83%
86.03%
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72

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NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELECOMMUNICATION INPORMATION:
TELEPAX: 703-836-620
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH 467 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: alinear
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700.00
84.66%
78.98%
                      ATTORNEY/AGENT INFORMATION:
 06-SEP-1995
                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-523-894-8
                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
FILING DATE: 06 CLASSIFICATION:
                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                       CCAGGTAAGGGTCTGGAGTGGATTGGTGAAATCAATCATAGTGGA---AGCACCAACTAC 246
                                                                                                                                                                                                                                                                                                                                            CTGAAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCGAGA----- 360
                                                                                                                                                                                                                                                                                                                                                                                                  -------GTAATTAGTTCGACCCTTGGGCCAGGGAACC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ArgProAspCysThrThrIleCysTyrGlyGlyTrpValAspValTrpGlyProGlyAsp 140
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APPLICANT: Hanna, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
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7
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
              Conservative:
Mismatches:
Indels:
                                                                                 US-08-728-463B-219 (1-524) x US-08-487-550-4 (1-476)
                                                         Gaps:
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GluPro 182
               Percent Similarity:
Best Local Similarity:
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COUNTRY: U
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133 TGCGCTGTCTATGGTGGTTCCTTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCA 189
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                                                                                                                                                                                                        21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08523894
Patent No. 6136110
GENERAL INFORMATION
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       475 GCCACAGGGGCCCTGGCTGGTCAAGGACTACTTCCCCGAACCG 522
467
139
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21
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                                      Conservative:
Mismatches:
Indels:
                                                                                                                                              US-08-728-463B-219 (1-524) x US-08-523-894-8 (1-467)
  Length:
Matches:
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190 CCAGGTAAGGGTCTGGAGTGGATTGGTGAAATCAATCATAGTGGAAGCACCAAĆTAC	61 ProGlyLygGlyLeuGluTrpIleGlySerPheTyrSerSerGlyAsnThrTyrTyr	Uy 24/ AAUCGICICTGAGAGTCGAGTCACATATGAGAACGTCCAGAACCAGTTCTT 306	Oy 307 CTGAAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCGAGA 360	Oy 361GTAATTAATTGGTTCGACCCTTGGGCAGGAACC 396	Qy 397 CTGGTCACCGTCTCCTCAACCCAAGGGCCCATGGGTCTTCCCCCTGGCACCTCC 456	Qy 457 TCCAAGAGCACCTGGGGCACAGCGGCCCTGGGCTGCTCAAGGACTACTTCCCC 516	GAACCG 522	Db 181 GluPro 182	550-4	; Sequence 4, Application US/08487550 ; Patent No. 6113898	on,	; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC ; TITLE OF INVENTION: TO HUMAN B1.1 AND/OR B1.2 PRIMATIZED FORMS THEREOF, ; TITLE OF INVENTION: PRARMACEUTIAL COMPOSITIONS CONTAINING. AND 15F THEREOF AS	IMMUNOSUPPRESANTS"	CORRESPONDENCE ADDRESS: ADDRESSE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street	Alexandria VA : IISA	231 REA	Compatible C-DOS/MS-DOS	E F E	G DATE: 07-JUN- IFICATION: 435 Y/AGENT INFORMAT	; NAME: Teskin, Robin L. ; REGISTRATION NUMBER: 35,030 ; REFRENCE/DOCKET NUMBER: 012712-131	H	K: 70 V FOR CHARA	476 ami amino a 3X: lin	; MOLECOLE TYPE: Drocein US-08-487-550-4	Alignment Scores: Pred. No.: 3.23e-63 Length: 476
Db 121 ValGlyLeuArgGlyGlyAsnTyrGlyMetAspValTrpGlyGlnGlyThrLeuValThr 140 Qy 406 GTCTCCTCAGCCTCAAGGGCCCATCGTCTTCCCCTGGCACCCTCTCTCAAGAG 465	Db 141 ValSerSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSer 160	Qy 466 ACCTCTGGGGGCACAGCGGCCCTGGGCTGGCTCAAGGACTACTTCCCGGAACCG 522	RESULT 3 US-08-487-550-12 ; Sequence 12, Application US/08487550	Patent No. 6113898 GENERAL INFORMATION: APPLICANT: Anderson, Darrell R. TTHIE OF INVENTION: TTHIE OF INVENTION: APPLICANT.		CORRESPONDE ADDRESSEE STREET:			#BDIUM TYPE: Floppy disk COMPUTER: ISH PC compatible				NAME: Teskin, Robin L. REGISTATION NUMBER: 35,030 REFERENCE/POCKET NIMBED: 013713	TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620	; INFORMATION FOR SEQ ID: ; SEQUENCE CHARACTERISTICS:	 LENGTH: 476 amino acids TYPE: amino acid TOPOLOGY: linear 	; MOLECULE TYPE: protein US-08-487-550-12	Length:	Percent Similarity: 739.00 Matches: 147 Percent Similarity: 85.16* Conservative: 8 Best Local Similarity: 80.77* Mismatches: 15 Ouery Match: 75.42* Tradal	3 Gaps:	-08-/28-46	Qy 13 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCTAGANGGGTCCTGTCTCAG 72	Qy 73 GTGCAGCTACAGCAGTGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCACC 132	133 TGCGCTGTCTATGGTGGTTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCA	

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133 TGCGCTGTCTATGGTGGTTCCTTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCA 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 yalGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAG
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                                                                                                                                                                                            APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                      467
1139
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21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                  ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 06-SEP-1995
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                     Sequence 12, Application US/08523894 Patent No. 6136310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.74e-61
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84.66%
78.98%
72.39%
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                                                                                                                                                                                                                                                                                                                                                                                           STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    703-836-202
                                                                                                                                                                                GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCGCTGTCTATGGTGGTTCCTTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCA 189
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|LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaSerAsnIle 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrGlySerGlyGlyThrAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 AACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGAACACGTCCAAGAACCAGTTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 CTGAAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCTAGATGGGTCCTGTCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- AGAGTAATTAATTGGTTCGACCCTTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
                                                                     CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER: ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/523,894
FILING DATE: 06-SEP-1995
TISSING DATE: 06-SEP-1995
TISSING DATE: 06-SEP-1995
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1139
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Conservative:
Mismatches:
Indels:
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NUMBER OF SEQUENCES: 59
CORRESBONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                           35,030
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                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.66%
78.98%
72.39%
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Best Local Similarity:
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Pred. No.:
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GENERAL INFORMATION:

APPLICANT: OPEER, Martin

APPLICANT: CEEK, Martin

APPLICANT: CZECH, Joerg

TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,

TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES

TITLE OF INVENTION: 1 N E. COLI

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             73 GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 132
                                                                                                                                                                             193 GGTAAGGGTCTGGAGTGGATTGGTGAAATCAATCATAGTGGAAGCACCAACTACAACCCG 252
                                                                                                                                                                                                                                                                                                                                     253 TCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTGTGAAA 312
                                                  1 MetlysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
                                                                                                                         9
                                                                                                                                                                                                   41 CysAlaValTyrGlyGlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProPro
                                                                                                                                                                                                                                                                              313 CTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCGAGA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION VUMBER: US/08/630,820 FILING DATE: 10-APF-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION WUMBER: DE 19513676.4
FILING DATE: 11-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANDOS, Particia D.
REGISTRATION VIMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 7, Application US/08630820 ; Patent No. 6008023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.31e-52
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20007-5109
ZIP: 20007-5109
COMPUTER REDABLE FORM:
MEDIUM TYPE: Flore
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INFORMATION FOR SEQ ID NO:
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Pred. No.:
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  AACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCT
                                                                                                                                                       ---AGAGTAATTAATTGGTTCGACCTTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 118, Application US/08545809A
Sequence 118, Application US/08545809A
BENERAL INFORMATION:
APPLICANT: Honjo.
APPLICANT: Honjo.
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                       161 SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 176
                                                                                                                                                                                                                                                                                                                475 GGCACAGCGGCCCTGGCTGCTGGTCAAGGACTACTTCCCCGAACCG 522
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Mismatches:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM: Windows95
SOFTWARE: Fast5EQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
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Matches:
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REGISTRATION NUMBER: 29,066
REFERENCE/OOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US/08/545,809A
27-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
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100.00%
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amino acid
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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22 SerlleAsnThrIleLeuTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 LeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GlyProGlyLeuValLysProSerGluAlaLeuSerLeuThrCysThrValSerGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 TCCTTCAGTGGT-----TACTACTGGAGCTGGATCCGCCAGCCACCAGGTAAGGGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 CGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTCTGAAACTGAGCTCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 GGCCAGGGAACCCTGGTCACCGTCTCAGCCTCAACCAAGGGCCCATCGGTCTTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 GAGTGGATTGGTGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCTCTCAAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS
TITLE OF INVENTION:
NUMBER OF SUGUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                     219
121
6
17
17
                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-728-463B-219 (1-524) x US-09-460-384-37 (1-219)
                                                               TAYAR=1A
                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                               NAME: YUN, Allen C
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: EL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 737-3528
   FILING DATE: 12-JUN-1997
                                                                                                                                                          LENGTH: 219 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08793450 Patent No. 6312690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              505 GACTACTTCCCCGAACCG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                         INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   5.6e-52
607.00
86.99%
82.88%
                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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US-08-793-450-4
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INVENTION: CD28/CTLA-4 INHIBITING PEPTIDOMIMETICS, PHARMACEUTICAL COMPOSITIONS THEREOF, AND METHOD OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                408
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                                                                                                                                            ACCTGCGCTGTCTATGGTGGTTCCTTC - - - AGTGGTTACTACTGGAGCTGGATCCGCCAG
                                                                                                                                                                                                            |||||||
|ThrCysThrValSerGlyPheThrIleSerSerGlyTyrSerTrpHisTrpValArgGln
                                                                                                                                                                                                                                                    CCACCAGGTAAGGGTCTGGAGTGGTGAAATCAATCATAGTGGAAGCACCAACTAC
                                                                                                                                                                                                                                                                                                                CTGAAACTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTGTGCGAGAGTA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 SerSerAlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThr
                                                                                                                         CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTC
                                                                                                                                                                                                                                                                       ----ATTAATTGG----TTCGACCCTTGGGGCCAGGGAACCCTG-----GTCACCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTCAGCCTCAACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTGGGGGCACAGCGGCCCTGGCTCCAAGGACTACTTCCCCGAACCG 522
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121
14
16
7
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Ste. 300
             Conservative:
Mismatches:
Indels:
                                                                                          US-08-728-463B-219 (1-524) x US-08-630-820-7 (1-832)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/12312
FILLIG DATE: 11-JUN-1998
APPLICATION NUMBER: US 60/049,470
 Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37, Application US/09460384
; Patent No. 6337316
; GENERAL INFORMATION:
HEL TAYAR; Nabil
BLEGGHNER, Steven
JAMESON, Brad
TEPPER, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 13-Dec-1999
CLASSIFICATION: <Unknown>
              85.44$
76.58$
62.82$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
             Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-460-384-37
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                                          Query Match
DB:
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linear
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 ThrCysThrValTyrGlyGlySerPhcSerGlyTyrTyrTrpSerTrplleArgGlnPro 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 ProGlyLysGlyLeuGluTrplleGlyGlulleAsnHisSerGlySerThrAsnTyrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
 SSEE: P.C.
I: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
ARLINGTON
                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION DATA:
APPLICATION DATE: P34/10566
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F:
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 660-118-0 PCT
TELEPHONE: 703-413-3000
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Matches:
Conservative:
Mismatches:
Indels:
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578.00
90.24%
88.62%
59.77%
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS.
                                                                                        ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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121 ValSerSer 123
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Best Local Similarity:
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                                            CITY: AR
STATE: V
COUNTRY:
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DB:
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RESULT 12

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GENERAL INFORMATION:
APPLICANT: MARAGOCO, Wayne A.
APPLICANT: MARAGOCO, Wayne A.
APPLICANT: HASELTINE, William A.
APPLICANT: HASELTINE, William A.
APPLICANT: HASELTINE, William A.
APPLICANT: HASELTINE, William A.
APPLICANT: HASELTINE, William A.
TITLE OF INVENTION: REACTIVE NEUTRALIZING HUMAN
TITLE OF INVENTION: ANTI-GP 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
CITY: BOSION
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 GTGCAGCTACAGCAGGGGGGGGGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC 132
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4411
602
602
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,774A
FILING DATE: US/09/480,774A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/400,674
FILING DATE: 08-MAR-1995
APPLICATION NUMBER: 07/804,652
FILING DATE: 08-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 34,235
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-728-463B-219 (1-524) x US-08-480-774A-2 (1-142)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
Indels:
Sequence 2, Application US/08480774A
Patent No. 5852186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 142 amino acids
amino acid
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85.92%
77.46%
58.43%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein FRAGMENT TYPE: internal
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101 TyralametAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLys 120
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                                                                                                                                                                                                                                                                                                                                                                                                             427 GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCCACAGGGCC 486
                                                                                                                                                            190 CCAGGTAAGGGTCTGGAGTGGTGAAATCAATCATAGTGGAAGCACCAACTACAAC 249
                                                                                                                                                                                                                                                                                                                            250 CCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCTCTG 309
                                                                                                    21 ThrCysThrValSerGlyPheSerLeuThrAsnTyrGlyValHisTrpValArgGlnSer 40
                                                                                                                                                                                                                                                                                                                                                                                                                                  370 TGG---TTCGACCCTTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCCTCAGCCTCAACCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08397411

Patent No. 6129914

GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Tso, 7 vun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California COURRY: USA ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 LeuGlyCysLeuValLysAspTyrPheProGluPro 152
                                        US-08-728-463B-219 (1-524) x US-08-397-411-6 (1-273)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Smith, William M.
REGIETRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-397-411-7
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GGTAAGGGTCTGGAGTGGATTGGTGAAATCATAGTGGAAGCACCAACTACAACCG 252
                   253 TCTCTCAAGAGTCGAGTCACATATCAGTAGACACGTCCAAGAACCAGTTCTCTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Link, Brian
TITLE OF INVENTION: Bispecific Antibody Effective
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.25
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Matches:
Conservative:
Mismatches:
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REGISTRATION UNMBER: 30,23
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
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Patent No. 6129914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  564.50
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75.66%
58.38%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 273 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
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ADDRESSEE: Townsend
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Best Local Similarity:
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-93
                                   TYPE: PRT
ORGANISM: Artificial Sequence
 SEQ ID NO 93
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APPLICANT: Emery, Stephen
APPLICANT: Emery, Clive Graham
APPLICANT: Copley, Clive Graham
APPLICANT: Copley, Clive Graham
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: GB9603103.3
PRIOR APPLICATION NUMBER: ED96-05-04
PRIOR FILING DATE: 1996-05-04
PRIOR FILING DATE: 1996-05-04
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ 1D NOS: 131
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                             70 CAGGTGCAGCTACAGCAGTGGGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                   190 CCAGGTAAGGGTCTGGAGTGGATTGGTGAAATCAATCATAGTGGAAGCACCAACTACAAC 249
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Conservative:
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             INPORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
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81.58%
75.66%
58.38%
 415-326-2422
                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
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Best Local Similarity:
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Pred. No.:
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TELEFAX:
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|LeuTrpLeuAsnTrpIlePheLeuValThrLeuLeuAsnGlyIleGlnCysGluValGln
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                                                                Percent Similarity:
Best Local Similarity:
Alignment Scores:
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Perfect score:

Sequence:

OM nucleic

9

Scoring table:

Searched:

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 840368
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40368
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-130 eXLB:
A;Cross-references: EMBL:X72478; NID:9441424; PIDN:CAA51146.1; PID:9441425
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
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Alignment Scores:
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                   - protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Database

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If kappa chain V-J region - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Accession: $40333

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 33, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: $40312; MUID:94080891; PMID:8258341

A;Accession: $403133

A;Accession: $403133

A;Residues: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-125 < KMLP.

A;Kesidues: 1-125 < KMLP.

A;Cross-references: EMBL:X72443; NID:9441354; PIDN:CAA51111.1; PID:9441355

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-108/Domain: immunoglobulin homology < IMM>
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C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
R;Rocca, Khamilchi, A.A.i Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, J.I.Cilin. Exp. Immunol. 91, 506-509, 1993
A;Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in light A;Reference number: A49134; MUID:93185310; PMID:7680298
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CCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGTGCCCATCAAGGTTCAGC
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A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-141 «ROC>
A;Cross-references: EMBL:X67322; NID:g33268; PIDN:CAA47736.1; PID:g33269
A;Cross-references: EMBL:X67322; NID:g33268; PIDN:CAA47736.1; PID:g33269
A;Note: sequence extracted from NCBI backbone (NCBIP:127088)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>
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                                             2 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAlaArgCys
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                            ATGATGGTCCCAGCTCAGCTCCTCGGTCTCTGCTGCTCTGGTTCCCAGGTTCCAGATGC
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
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C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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R,Klein, R.; Jaenichen, R.; Zachau, H.G.

R,Klein, R.; Jaenichen, R.; Zachau, H.G.

R,Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:94080891; PMID:8258341

A;Stacession: $40334

A;Stacus: preliminary; translation not shown

A;Molecule type: mRNA
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A;Cross-references: EMBL:X72444
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterzamer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>
A;Molecule type: mRNA
A;Residues: 1-125 <KLES
A;Croses-references: EMBL:X72426
C;Superfamily: immonoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                    US-08-728-463B-220 (1-420) x S40316 (1-125)
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586.00
93.89%
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77.00%
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93.60$
90.40$
77.14$
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Best Local Similarity:
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Pred. No.:
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141

Db 63 GlyLysAlaProLysLeuLeulleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 82 Qy 253 AGGTCAGCGGAACTGGACACATTCACTCTCACCATCAGCAGCCTCACCATCAGCAGCTT 312 By ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 102 Qy 313 GAAGATTTCCAACTTACTATTGTCAACAGGCTAATAGTTTCCCG 357	Alignment Scores: 1.71e-42 Length: 117 Pred. No.: 574.00 Matches: 109 Score: 574.00 Matches: 109 Best Local Similarity: 93.164 Mismatches: 5 Query Match: 75.434 Indels: 0 US-08-728-463B-220 (1-420) x S46376 (1-117)	Qy 46 CTGCTCTGGTTCCCAGGTTCCAGATGCCAATGACCAGTCTCCATCTTCCGTG 105 Db 1 LeuLeuTrpPheProGlySerArgCysAsplleGlnMetThrGlnSerProSerSerVal 20 Qy 106 TCTGCATCTGTAGGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGATATTAGCAGC 165 Db 21 SerAlaSerIleGlyAspArgValThrIleH	226 TCCAGTTTGCAAAGGTCCCATCAAGGTTCAGGGAAGTGGAACTGGAAGATTTC	RESULT 9 \$40352 Ig kappa chain V-J-C region - human C;Species: Homo sapiens (man) C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C;Accession: S40352 R;Klein, R.; Jaenichen, R.; Zachau, H.G. Eur. J. Immunol. 23, 32484-3271, 1993 A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
Oy 262 GGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGAAGATTT 321	A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989 R; Wagner, S.D.; Luzzatto, L. Bur. J. Immunol. 23, 391-397, 1993 A; Title: V. Kappa gene segments rearranged in chronic lymphocytic leukemia are distribute A; Reference number: 834076; MUID:93170387; PMID:8436174 A; Accession: 834076 A; Molecule type: DNA A; Residues: 30-117 < WA2> A; Cross-references: EMBL:X66044; NID:933320; PIDN:CAA46843.1; PID:933321; EMBL:X66043; N A; Experimental course.	A;Accession: 334105 A;Molecule type: DNA A;Residues: 30-117 < WAG> A;Residues: 30-117 < WAG> A;Residues: 30-117 < WAG> A;Residues: 30-117 < WAG> A;Residues: 30-117 < WAG> A;Residues: 30-117 < WAG> A;Residues: 30-117 < WAG> A;Reperimental source: patient 8 C;Genetical Source: patient 8 A;Introns: 19/1 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology < IMM>	Alignment Scores: Alignment Scores: Score: Score: Score: Secre:	

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133 ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 192
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                                                                                                                                                                                                                                                                                                                             82 LysPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 101
                                                                                                                                                                                                                                                                                                                                                                                                142 CGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCAGGTAAAGCA 201
                                                                                                                                                                                            42 IleThrCysArgAlaSerHisValIleSerAsnHisLeuValTrpPheGlnGlnLysPro 61
                                                                                                                                                                                                                                                          62 GlyLysAlaProLysSerLeulleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 81
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C;Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: $40349
Evr. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID: 94080891; PMID: 8258341
A;Accession: $40349
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC
                                                                                                                         22 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr
                                                                                                                                                                                                                                                                                                                                                                              GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAG
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                                        13 ATGATGGTCCCAGCTCAGCTCCTCGGTCTCCTGCTCTGGTTCCCAGGTTCCAGATGC
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       US-08-728-463B-220 (1-420) x S40369 (1-129)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAACCAAGCTGGAGATCAAACGA 396
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R. Klein, R.; Jaenichen, R.; Zachau, H.G.

Bur. J. Immunol. 23, 3248-3271, 1993
A.Title: Rxpressed human immunoglobulin chi genes and their hypermutation. A; Reference number: 840312; MUID: 94080891; PMID: 8258341
A; Accession: S40369
A; Status: preliminary; translation not shown A; Residues: 1-129 «KLE»
A; CCOSG-references: EMBI.x777770...
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-131 <KLE>
A;Cross-references: EMBL:X72462; NID:g441392; PIDN:CAA51130.1; PID:g441393
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                             133 ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 IleThrCysArgAlaSerGlnGlyIleSerAsnTyrLeuAlaTrpTyrGlnGlnLysPro
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                                                                                                                                                                                                                                                                                                             ATGATGGTCCCAGCTCCACCTCCGTCTCCTGCTCTCGGTTCCCAGGTTCCAGATGC
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                                                                                                                                                                                           C'Species: Homo sapiens (man)
C'Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C'Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C'Accession: 840313
R'Klain, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A'Tille: Expressed human immunoglobulin chi genes and their hypermutation. A'Reference number: 840312; MUID:9408091; PMID:8258341
                                                                 GCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGGTACACTTTTGGTCAGGGAACCAAG
                                                                                                                                                                                                                                                                                             A.Molecule type: mRNA

A.Kesidues: 1-123 - «KLES

A.Kesidues: 1-123 - «KLES

A.Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351

C.Superfamily: immunoglobulin V region; immunoglobulin homology

C.Keywords: heterotetramer; immunoglobulin

F;32-106/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTCAGCTCCTCGGTCTCTGGTTCCCAGGTTCCAGATGCGACATCCAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 ACCCAGTCTCCATCTTCCGTGTCTGTAGGAGACAGAGTCACCATCACTTGTCGG
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562.00
93.50%
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Best Local Similarity:
Query Match:
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 61
                       262
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RESULT 13 S46372

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IG Hight chain variable region (VJ) - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: O'O-May-1955 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C; Accession: S46372
R; Bensimon, C: Chastagner, P: Zouali, M.
R; Bensimon, C: Chastagner, P: Zouali, M.
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>
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R;Bensimon, C.; Chastagner, P.; Zouali, M.
Submitted to the EMBL Data Library, November 1993
A;Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A;Reference number: S38643
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Species: Homo sapiens (man)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
                                                                                                                                        CAGCTCCTCGGTCTCCTGCTGCTCTGGTTCCCAGGTTCCAGATGCGACATCCAGATGACC
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A/Molecule type: mRNA
A/Residues: 1.132 & DENN-
A/Residues: 1.132 & DENN-
A/Cross-references: EMBL: Z27173; NID:g415961; PIDN:CAA81697.1; PID:g415962
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/40-114/Domain: immunoglobulin homology <IMM>
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13-AUG-1987 (Rel. 05, Last sequence update)
15-AUG-1999 (Rel. 38, Last annotation update)
15 AUG-1999 (Rel. 38, Last annotation update)
16 Aappa chain V-I region Walker precursor.
Homo sapins (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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P01595
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KV1W HUMAN
ID KV1W HUMAN
AC P04431;
     Command line parameters:
-MODEL=frame+ n2p model - DEV=xlp
-MODEL=frame+ n2p model - DEV=xlp
-MODEL=frame+ n2p model - DEV=xlp
-DES-SA'SEPTO_SPOOJ/US08728463/runat 03062003_085614_16804/app_query.fasta_1.3690
-DES-SA'SEPTOC_40 - OFMT=fastan - SUFFIX=xEP - MINMATCH=0.1 - LOOPCL=0 - LOOPEXT=0
-DES-SA'SEPTOC_40 - OFMT=fastan - SUFFIX=xEP - MINMATCH=0.1 - LOOPCL=0 - LOOPEXT=0
-UNITS-EDIG - START=1 - END=-1 - MATRIX=DIGSUMG_2 - TRANS=Dimman40 .cdi - LIST=45
-DOCALIGN=200 - THR SCORE=pct - THR MAX=DIGSUMG_3 085614_16804 - NCPU=6 - ICPU=3
-USER-SCORES-60 - MAIT - LOSPELOCK=100 - LONGLOG
-NO MWAP - LARGEQUERY - NEG_SCORES-0 - WAIT - DEPELOCK=100 - LONGLOG
-DEV_TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPEXT=0 - XGAPEXT=0.5 - FGAPED=6
-FGAPEXT=7 - YGAPEDP=10 - YGAPEXT=0.5 - DELOP=6
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InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
IMMUNOGLOBULI V region; Signal.
SIGNAL
     EMBL; J00245; AAAS9087.1; -.
EMBL; Z00001; CAA77292.1; -.
PIR; A01882; KIHU12.
HSSP; P01607; 1REI.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                      133 ATCACTTGTCGGCCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 192
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MEDLINE=81098966; PubMed=6779204;
Bentley D.L., Rabbitts T.H.;
Human immunoglobulin variable region genes -- DNA sequences of two V kappa genes and a pseudogene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
               COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
                                                            MW; F941FA07D4AFC2F9 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annocation update)
19 kappa chain V-I region HK102 precursor (Fragment).
Homo sapiens (Human).
                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                       SIMILARITY.
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     FRAMEWORK-3.
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RESULT 2

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193 GGTAAAGCACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGTGTCCCATCA 252
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Bentley D.L., Rabbitts T.H.;
"Human immunoglobulin variable region genes -- DNA sequences of two
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-I region HK101 precursor (Fragment).
Homo sapiens (Human)
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarkhini; Hominidae; Homo.
IG KAPPA CHAIN V-I REGION HK102.
FRAMEWORK-1.
                                           COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-3.
BY SIMILARITY.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                     13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15 August chain V-I region Daudi precursor.
16 Kappa chain V-I region Daudi precursor.
17 Homo sapiens (Human).
18 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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103 GluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerTyrPro 117
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PIR; A01884; K1HUDI.
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InterPro; IPR003596; Ig_v.
Efam; PF00047; ig; 1.
SWART; SM00466; IGv. 1.
Immunoglobulin V region; Signal.
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Best Local Similarity:
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                                                                                                                          KV1X HUMAN
P04432;
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                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                    SEQUENCE FROM N.A. MEDLINE-81129397; PubMed=6402305; MEDLINE-81129397; Pubmed=6402305; Meditor D.L., Rabbitts T.H.; "Evolution of immunoglobulin V genes: evidence indicating that recently duplicated human V kappa sequences have diverged by gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAPPA CHAIN V-I REGION HK101.
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PRAMENORK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMENORK-2.
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FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
BY SIMILARITY.
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Mismatches:
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HSSP, P01607; IREI.
InterPro; IPR0033066; Ig_MHC.
InterPro; IPR003306; Ig_W.
Ffam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
     cappa genes and a pseudogene.";
Nature 288:730-733(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12799 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; K01322; AAA58930.1; -. EMBL; K01324; AAA58932.1; -. EMBL; V00558; CAA23824.1; -.
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523.00
92.17%
89.57%
68.73%
                                                                                                                                                                                                                        Cell 32:181-189(1983).
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Best Local Similarity:
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                                                                                                                                              GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAG 372
                                                                                                                                                          61 ArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro
                                                                                            AGGTTCAGCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=81052342; PubMed=6776411;
Altenburger W., Steinmetz M., Zachau H.G.;
"Functional and non-functional joining in immunoglobulin light chain genes of a mouse myeloma.";
Nature 287:603-607(1980).
                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-Muspa chain V-V region T1 precursor.
Mus musculus (Mouse)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG KAPPA CHAIN V-V REGION TI.
PRAMEMORK-I.
COMPLEMENTARITY-DETERMINING-I.
PRAMEMORK-2.
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COMPLEMENTARITY-DETERMINING-3.
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Matches:
Conservative:
Mismatches:
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101 GlyThrThrValAspIleLysArg 108
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InterPro; IPR003006; Ig MHC.
InterPro; IPR003006; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
IMMUNOGlobulin V region; Signal.
SIGNAL
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478.00
82.81%
68.75%
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Best Local Similarity:
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P01637;
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Pred. No.:
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                            AGGTTCAGCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
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Wes)."
Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598 (1980).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR, A01877; KIHUWS.
HSSP, P80362; IWTL.
InterPro; IPR03006; Ig_MHC.
InterPro; IPR03066; Ig_V.
Pfam; PF0047; Mg; 1.
SWART; SM0406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein.
InterPro; IPR0301596; Ig_V.
FRAMEWORK-1.
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-81092279; PubMed-6778806;
Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
Preparative separation of the tryptic hydrolysate of a protein lighib-pressure liquid chromatography. The primary structure of a monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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FRAMEWORK-4.
BY SIMILARITY.
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Matches:
Conservative:
Mismatches:
Indels:
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-I region Wes.
Homo sapiens (Human).
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                                                                                                                                                                  373 GGAACCAAGCTGGAGATCAAA 393
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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93.52%
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US-08-728-463B-220 (1-420) x KV1D_HUMAN (1-107)
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56 CO
88 FR
97 CO
107 FR
108 BY
11671 MW;
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92.59%
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Milstein C.P., Deverson E.V.; "Primary structure of kappa light chain from a human myeloma protein.";
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INTERPROJ IPRO03006; Ig_MHC.
InterPro; IPRO03006; Ig_V.
InterPro; IRRONA; Ig_V.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Glycoprotein.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region CAR.
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73 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTTGCATCTGTAGGAGACAGAGTCACC 132
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"The primary structure of a monoclonal kappa-type immunoglobulin I
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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thope-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region Hau.
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HSSP; P80362; 1WTL.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_V.
Pfan; PP00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Bence-Jones pri
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13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-I region BAN.
Homo sapiens (Human)
Mararyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
MO1. Immunol. 23:73-78(1986).
PIR; A01878; K1HUBN.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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InterPro; IPR003006; Ig_MHC.
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"The primary structure of the Bence-Jones protein Kue. The amino acid sequence of the variable part of a human L-chain of the kappa-type.";
Hoppe-Seyler's Z. Physiol. Chem. 20(7.25-734(1979).
-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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FRAMEWORK-3.
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15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Kue.
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HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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1-JUL-1998 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-I region Rei.
17 kappa chain V-I region Rei.
18 kappa chains (Human).
19 kapyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Palm W., Hilschmann N.;
"The primary structure of a crystalline monoclonal immunoglobulin
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Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
"The molecular structure of a dimer composed of the variable of
of the Bence-Jones protein REI refined at 2.0-A resolution.";
Blochemistry 14:4952(1975).
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Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975)
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PDB; 1REI; 17-FEB-84.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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A Gall W.E., Edelman G.M.;

The covalent structure a human gamma G-immunoglobulin. X.

Intrachain disulfide bonds.";

Intrachain disulfide bonds.";

I. Biochemistry 9:3188-3196(1970).

-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=71064023; PubMed=5489770;
Gottlibe P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VI..
acid sequence of the light chain.";
Biochemistry 9:3155-3161(1970).
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FRAMEWORK-2.
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
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19 kappa chain V-I region EU.
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WEDLINE=83273707; PubMed=6410398;
WEDLINE=83273707; PubMed=6410398;
A Gonl F., Frangione B.;
A Gonl F., Frangione B.;
Thaino acid sequence of the Fv region of a human monoclonal IgM
Torcein WEA) with antibody activity against 3.4-pyruvylated
Torcein WEA) with antibody activity against 3.4-pyruvylated
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Torcein WEA with antibody activity against 3.4-pyruvylated
Torcein WEA with antibody activity against 3.4-pyruvylated
Torcein WEA Sol. Sci. U.S.A. 80.4837-4841[1983].
Torcein WEA DATINED FROM A MONOCLONAL ANTIBODY
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COMPLEMENTARITY-DETERMINING-1.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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AC PO159;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1999 (Rel. 38, Last annotation update)
DF 15-JUL-1999 (Rel. 38, Last annotation update)
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KVIR (REL OL), Created)
21-JUL-1986 (Rel. Ol, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-MUR-1999 (Rel. 38, Last annotation update)
16-MUR-1999 (Rel. 38, Last annotation update)
17-MUR-1999 (Rel. 38, Last annotation update)
18-MUR-1999 (MURAN).

ENARTYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                   FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
   COMPLEMENTARITY-DETERMINING-1
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                                                 MEDLINE=75059122; PubMed=4215718;
Laure C.J., Watanabe S., Hilschmann N.;
Laure C.J., Watanabe S., Hilschmann N.;
The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), I. The amino acid sequence of the L-chain of
kappa-type, subgroup I.";
Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN.
    Eukaryòta, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-3.
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HSSP, P01607; IREL.
INTERPRO; IPR001306; Ig_MHC.
INTERPRO; IPR001306; Ig_V.
Pfam; PF00047; ig; 1.
SWART; SM00406; IGV; 1.
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                        Bence-Jones protein Au.";
Biophys. Struct. Mech. 1:139-146(1975).
-!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF THE KAPPA CHAIN REI.
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                Schiechl H., Hilschmann N.; "Rule of a monoclonal "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones procein Au).";
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region AU.
Indoo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                         MEDLINE=77022433; PubMed=1234024;
Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman B.E.,
Schwager P., Steigemann W., Schramm H.J.;
"The structure determination of the variable portion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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HSSP; P01607; IREI.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig-V.
Pfam; PP00047; ig; I.
SMART; SM00406; IGV; I.
Immunoglobulin V region; Bence-Jones pr
                                                                                                                                        SEQUENCE.
MEDLINE=72189444; PubMed=5028201;
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81 GluAspileAlaThrTyrTyrCysGlnGlnTyrAspTyrLeuProTrpThrPheGlyGln 100 QQ

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Search completed: June 3, 2003, 09:04:11 Job time: 9.96662 secs

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Q8vci6 mus musculu Q9/184 mus musculu Q9/184 mus musculu Q8vc55 mus musculu Q8vc56 mus musculu Q8vc186 mus musculu Q8rc18 mus musculu Q8rc29 mus musculu Q9/140 achi stooma Q9/174 mus musculu Q9/176 mus musculu Q9/176 mus musculu Q9/176 mus musculu Q9/180 homo sapien Q91180 homo sapien Q91029 homo sapien Q91029 homo sapien Q91029 homo sapien Q91029 homo sapien Q91029 homo sapien Q91029 homo sapien Q91020 homo sapien Q91020 homo sapien Q91020 homo sapien Q91020 homo sapien Q91020 homo sapien Q91020 homo sapien Q91020 homo sapien Q91020 homo sapien Q91020 homo sapien Q91020 homo sapien Q91020 homo sapien
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Q9qyf0 mus m
Q99m37 mus m
Q91183 homo s
Q92066 mus m
Q9vij0 mus m
Q9uj178 homo s
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      liscur-creen.;
Strandberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027418; AAH27418.1; -.
Hypothetical protein.
SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEABI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234
97
14
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
Conservative:
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Q9JL76
Q9JL80
Q9JL82
Q9JL82
                                                                                                                                                Q925S9
Q8TCD0
Q9UL77
Q91WF8
Q8VCP0
Q9UL70
Q96SA9
Q9UL79
Q96FF6
Q91WS9
Q91WS9
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Q99M37
Q9UL83
Q920E6
Q8VIJ0
Q9UL78
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Q9JL84
Q920E9
Q8VC55
Q8VDD0
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Q8R028
Q9ERZ9
Q9U410
Q91W12
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82.22%
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SEQUENCE FROM N.A.
TISSUE=COLON;
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Percent Similarity:
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230.5
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Q8R062;
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-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-DE-SPTEMBL 21 / OFFTO spool/US08728463/runat 03062003 085614 16815/app_query.fasta_1.3690
-DB-SPTEMBL 21 - OFFTT=68tan - SUFFTIS=rspt -MINMATCH=0.1 -LOOPCL=0. LOOPCL=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blooum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM==ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USR=US08728463 @CGN 1 1.380 @runat 0306203 085614 16815 -NCD=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGICG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                 AAGCTTGCCACCATGATGGT............TGGCTGCACCATCTGTCTTC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                              3, 2003, 08:56:26 ; Search time 37.2838 Seconds
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                             OM nucleic - protein search, using frame_plus_n2p model
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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sp_mammal:*
sp_mhc:*
sp_nter:*
sp_phage:*
sp_phage:*
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sp_bacteriap:*
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761
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sp_bacteria:*
sp_fungi:*
sp_human:*
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Maximum DB seq length: 200000000
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Match Length DB
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GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 132
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                                                                                        133 ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 192
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                                                              20
                                                                                                      21 IleThrCysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnLysPro 40
                                                                                                                                                           41 GlyLysAlaProAsnLeuLleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60
                                                                                                                                                                                                                 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
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                                                 253 AGGITCAGCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Strausberg R.;
L Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
E BML; GC015292, AAH15292.1;
R InterPro; IPR001306; Ig MHC.
R InterPro; IPR001306; Ig MHC.
R InterPro; IPR00145; Ribosomal_S2.
R PERM; PROO147; ig; 2.
R PROSITE; PS00290; IG MHC; UNKNOWN 1.
R PROSITE; PS00290; IG MHC; UNKNOWN 1.
RROSITE; PS00962; RIBOSOWAL_S2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; BODOBOEGEB7812D2 CRC64;
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O91WF8
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DAR-2002 (TrEMBLrel. 20, Last annotation update)
Hyporhetical 25, 9 kba protein.
Mus musculus (Mouse).
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Matches:
Conservative:
Mismatches:
       US-08-728-463B-220 (1-420) x Q9UL77 (1-108)
                                                                                                                                                                                                                                                                                                                        US-08-728-463B-220 (1-420) x Q91WF8 (1-234)
                                                                                                                                                                                                                                                                                                           GGAACCAAGCTGGAGATCAAACGA 396
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485.00
82.22$
70.37$
63.73$
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TISSUE=COLON;
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Best Local Similarity:
Query Match:
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                                                                                                 21 AspileGlnMetThrGlnThrThrSerSerLeuSerAlaSerLeuGlyAspArgValThr
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                                                                                 ATGATGGTCCCAGGTCCCTCGTCTCCTGCTCTGGTTCCCAGGTTCCAGATGC
                                                                                                                                                                                                                                                                                                       AGGTTCAGCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
BEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                              GGAACCAAGCTGGAGATCAAACGAACTGTGGGCTGCACCATCTGTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
11738 MW; C06681716C4D16F3 CRC64;
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95
6
7
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Matches:
Conservative:
Mismatches:
Gaps:
  Mismatches:
Indels:
Gaps:
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Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL, POLGO7, 1REI.
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                                                    US-08-728-463B-220 (1-420) x Q8R062 (1-234)
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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486.00
93.52%
87.96%
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  71.85%
64.65%
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108 AA;
Best Local Similarity:
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Best Local Similarity:
Query Match:
DB:
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SEQUENCE
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              Query Match:
DB:
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GGTAAAGCACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGTGTCCCATCA 252
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                                                                                               253 AGGTTCAGCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98277139; PubMed=9614934; Wal X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                    373 GGAACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTC
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035044; AAD56280.1; --
HSSP; P01607; IREI.
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
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91.67%
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                                       AspGlyThrValLysLeuLeuIleTyrTyrThrSerArgLeuTyrLeuGlyValProSer 80
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01-MRA-2002 (TrEMBLrel. 20, Created)
01-MRA-2002 (TrEMBLrel. 21, Last sequence update)
01-JUD-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.7 kDa protein.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUB-COLON;
Strausberg R.;
Strausberg R.;
Submitted (BC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019474; AAH19474.1;
Interpro; IPR001599; Ig.
Interpro; IPR003597; Ig.cl.
Interpro; IPR003596; Ig.W.
Interpro; IPR003596; Ig.V.
Ffam; PF00047; Igi. 2.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00407; IGG1; 1.
SWART; SM00407; IGG1; 1.
                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;
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Myosin-reactive immunoglobulin light chain variable region
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                             Homo sapiens (Human)
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SEQUENCE FROM N.A.
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A Adderson E. B., Shikhman A.R., Ward K.E., Cunningham M.W.;
A Adderson E.B., Shikhman A.R., Ward K.E., Cunningham M.W.;
Andlecular analysis of polyreactive monoclonal antibodies from rhoumatic carditis: human anti-N-acetylglucosamine/anti-myosin T rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin T unibody V region genes.";
J. Immunol. 16:1202-2031[1998].
R EMBL; U96396; AAB68785.1: -
R InterPro; IPR003006; Ig_MHC.
R FEMBL; U96396; Ig_MHC.
R FEMBL; U073006; Ig_MHC.
T NON TER 107 107
C SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).
Homo sapiens (Human)
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Last sequence update)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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            101 GlyThrLygLeuGlulleLygArg 108
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 GGAACCAAGCTGGAGATCAAACGA 396
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475.50
92.59%
88.89%
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Q9UL79;
01-MAY-2000 (TEMBLEEL 13,
01-MAY-2000 (TEMBLEEL 13,
01-DEC-2001 (TEMBLEEL 19,
                                                                         PRELIMINARY;
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
373
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                   SEQUENCE FROM N.A.

BEDLINE-98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB5845F19724FB4E CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
10-DEC-2002 (TrEMBLrel. 20, Last annotation update)
Kappa 1 light chain variable region (Fragment).
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Mismatches:
Indels:
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EMBL; AF036035; AAD56271.1;
HSSP; PO1607; IREI.
InterPro; IPR003506; Ig_WHC.
InterPro; IPR003596; Ig_v.
Pfam; PR00047; Ig, 1.
NON_TER.
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Matches:
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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comenzô R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.; "The tropism of organ involvement in primary systemic amyloidosis: contributions of Ig V(L) germ line gene use and clonal plasma cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC_2001 (TrEMBLrel. 19, Created)
01-DEC_2001 (TrEMBLrel. 19, Last sequence update)
01-DEC_2001 (TrEMBLrel. 19, Last sequence update)
01-MAR_2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 25.8 kDa protein (Fragment).
Whan musculus (Mouse)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Muscl_TaxID=10090;
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TISSUB-COLON;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databages.
EMBL; BC013496; AAH13496.1; -.
InterPro; IRPO306; Ig_MHC.
Pfam; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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87
13
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Matches:
Conservative:
Mismatches:
Indels:
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  WEDLINE=21361171; PubMed=11468171;
                                                                        burden.";
Blood 98:714-720(2001).
BMBL; AF361758; AAK51465.1; -.
InterPro; IPR003006; Ig_MHC.
Pfam: PF00047; ig; 1.
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116 AA; 12735 MW;
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457.00
86.21%
75.00%
60.05%
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Best Local Similarity:
Query Match:
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SEQUENCE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MUX., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
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90
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
 Length:
Matches:
Conservative:
Mismatches:
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Mismatches:
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EMBL, AF035033, AAD56269.1; -.
HSSP, P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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Matches:
                                                                      Indels:
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                                                                                      Gaps:
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1.95e-42
453.00
81.60%
71.20%
59.53%
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450.50
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107 AA;
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                                    Percent Similarity:
Best Local Similarity:
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133 ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 192
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                                                                                                                                                                                                                                                  61 AspGlyThr1leLy8ArgLeulleTyrAlaThrSerSerLeuGlySerGlyValProLy8 80
                                                                                                                                                                                                                                                                                                         GAAGATITIGCAACTIACTATIGICAACAGGCTAATAGTTICCCGGTACACTITIGGTCAG 372
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        21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
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                                                                             253 AGGTICAGCGGAAGIGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26.2 kDa protein.
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TISSUE=LUNG;
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MEDLINE=99306687, PubMed=10380019;

A Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
A Propathi P.K., Chatterjee S.K.;

"Construction and characterization of a chimeric fusion protein
T constanting of an anti-idiotype antibody mimicking a breast cancer-
T constanting of an anti-idiotype antibody mimicking a breast cancer-
T sessoiated antigen and the cytokine GM-CSF.";
Hybridoma 18:193-202(1999).
R EMBL; AF124721; AAK55120.1;
R Pfan: PF0047; 1g; 1.
T NON_TER 127

SEQUENCE 127 AA; 13794 MW; 13F61BEBBB981FA5 CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Immunoglobulin light chain (Fragment)
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Interpro; IPR003606; Ig_Nke.
Interpro; IPR003606; Ig_WHC.
Interpro; IPR003596; Ig_v.
Pfam; PF00047; Ig.2
SMART; SM00409; IG.2
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Submitted (JAN-2001)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-UIN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 26.3 kDa protein:
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Best Local Similarity:
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SMART; SM00406; IGv; 1.

SMART; SM00410; IG like; 1.

PROSITE; PS00290; IG MHC; UNKNOWN 1.

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"Cloning of cDNAs encoding for anti-white pine blister rust mantibody (Mab 7, its light and heavy chains) and construction single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFLS2371; ADA040242.1; -
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Kappa light chain of Mab7 (Fragment).
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  GluAspMetGlyIleTyrTyrCysLeuGlnTyrAspGluPheProPheThrPheGlySer
                         GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAG
                                                                                                                    AGGTTCAGCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                            GlyLysSerProLysThrLeuIleTyrArgAlaAsnArgLeuValAspGlyValProSer
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                                                                                    ArgPheSerGlySerGlySerGlyGlnAspTyrSerLeuThrIl
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STRAIN=BALB/C; TISSUE=SPLEEN;
MEDLINE=20183931; PubMed=10706631;
Shinohara N., Demura T., Fukuda H.;
"Isolation of a vascular cell wall-specific monoclonal antibody "Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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SMART; SM00406; IGv; 2.
SEQUENCE 298 AA; 318
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HSSP; P01607; 1REI
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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-DB=A Geneseq_101002 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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2002 (first entry) man AILIM monoclonal antibody clone Jmab-136, light chain. antirheumatic; antiarthritic; antidiabetic; antipsoriatic; ergic; antiulcer; neuroprotective; antithyroid; vasotropic; suppressive; dermatological; antiinflammatory; hepatotropic; ion inducible lymphocyte immunomodulatory molecule; AILIM; shall antibody; allergy; rheumatoid arthritis; diabetes mellitus; esclerosis; autoimmune thyroiditis; psoriasis; hepatitis; contact-type dermatis; chronic inflammatory dermatosis; clupus erythematosus; autoimmune disorder; inflammation; rersus host reaction; immune rejection; intestinal immunity;			236 AA.	ALIGNMENTS	AAR54053 AAW90931	ABB74901 AAB03684	AAW90932	AAY56724 ARC1 8767	AAW90930 ABB74899	AAR13050	AAR92085	AAB03713 AAR57482	AAR65018 AAR87057	AAW11640	AAW10233	AAY56722	AAM47645	AAR77614 ABP51696	AAY56723	AAY96293	AAW24990 AAY56737	AAW01527	AAR42065	AAY96297 AAB15546	AAW11638	AAR20058 AAB99115	ABP41164	AAY96301 ABP43157	AAY96289	AAR38162 AAY96298	B 7	ID
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                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel human antibody (I), preferably a human CC monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (I) is useful for modulating signal CC transduction into a cell mediated by AILIM, for modulating signal CC af AILIM-expressing cells, for modulating production of a cytokine from CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity (CC AILIM-expressing cells and/or immune cytolysis or apoptosis of CC prophylaxis of delayed type allergy. (I) is useful for treating, preventing or CC prophylaxis of delayed type allergy. (I) is useful for treating and CC costimulatory transduction, and for inhibiting the onset and/or advancement of the diseases associated with AILIM-mediated (CC costimulatory dermatosis, allergic contact-type dermatitis, CC cinsulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic contact-type dermaticis, CC disorders, inflammation, graft versus host reaction, graft versus host reaction, graft versus host caction, graft versus host caction, graft versus host caction, graft versus host caction, graft versus host caction, graft versus host caction, graft versus host caction, graft versus host caction, graft versus host caction, graft versus host caction, graft versus host caction, graft versus host caction, graft versus host caction, graft versus host caction, disorders such as contact-type dermatitis, and contact-type dermatitis, and contact-type dermatitis, and contact-type dermatitis, and contact-type dermatitis, and contact-type dermatitis, and contact-type dermatitis, and contact-type dermatitis, and contact-type dermatitis, contact-type dermatitis, contact-type dermaticity (HAMA) in a host.
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cell proliferation; cancer; anti-HIV; antiallergic;
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/note= "Ig MHC motif"
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infection; inflammation; haematopoiesis; AIDS; allergy.
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                                                                                                   IleThrCysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnLysPro
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                        US-08-728-463B-220 (1-420) x AAY96298 (1-237)
                                                                                                                                                                                                                                                                                                                                  The present sequence is the human immunoglobulin superfamily protein CC IGFAM-10. Its gene was isolated from a cDNA library of colon CC tissue. It is expressed in reproductive, gastrointestinal and CC cardiovascular tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for CC diagnosing and treating many diseases, including cancer, immune system CC disorders (such as inflammation, AIDS, allergies, anaemia, CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, CC multiple sclerosis, shoriasis, rheumatoid arthritis, scleroderma, CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, CC systemic lupus crythematosus and ulcerative colitis, complications of CC cancer, haemodialysis and extracorporeal circulation, trauma and CC haematopoietic cancer (such as leukaemia) and infections caused by CC bacteria, viruses, fungi or parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated will altered levels of the protein such as cancer, immune system disorders
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N-PSDB; AAA27390.
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response proteins (HIRP), the polynucleotides encoding them, and the use of these compositions for the diagnosis, treatment or compositions for the diagnosis, treatment or compositions for the diagnosis, treatment or compositions for the diagnosis, treatment or compositions for the diagnosis, treatment or compositions for the diagnosis, treatment or compositions for the diagnosis, treatment or compositions for the diagnosis, treatment or compositions of the present sequence is that of human immune response protein 1 compositions of the protein of compositions of the composition of the diagnosis of the composition of call, to an HIV-1 antigen binding protein, and composition of compositions of the composition of compositions of the diagnosis of the composition of cell proliferative disorders (e.g. connective tissue disease (MCTD), myelofibrosis, bursitis, mixed leukaemia, hepatitis, cirrhosis and atherosclerosis). and compositatory disorders e.g. AIDS and atherosclerosis).
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                                                                                                                                                                                                                                                                 No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human immune response proteins, for treating immunological disorders and cell proliferative disorders, and for assessing the effects of exogenous compounds on the expression of HIRP molecules
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22-DEC-1998;
07-APR-1999;
                 The present sequence is the human immunoglobulin superfamily protein IGFAM-1. Its gene was isolated from a cDNA library of synovial membra tissue. It is expressed in reproductive, gastrointestinal and cardiovascular tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable
   gene, protein, diagnosing and
                                                                                                                                                               Immunoglobulin superfamily proteins, the agonist and antagonist of protein is useful for preventing and treating disorders associated altered levels of the protein such as cancer, immune system disorder
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ion; inflammation; haematopoiesis; AIDS; allergy.
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98US-0113635.
99US-0128194.
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 treating many
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215..232
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Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                  English.
   diseases,
                                                                                                                                                                                                                                                                                    Guegler Yang J;
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 including
                                                                                                                                                                                                                                                                                                     Gorgone GA,
                                                                                                                                                                   system disorders
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   system
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative colitis), complications cancer, haemodialysis and extracorporeal circulation, trauma and haematopoietic cancer (such as leukaemia) and infections caused by
                                                                                                                                                                                                                                                     Human IGFAM-13 immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                       AAY96301;
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                   Domain
                                                  Domain
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                                                                                                                Peptide
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                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                  infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                    immunoglobulin; IGFAM-13; IGFAM; immune
ion; inflammation; haematopoiesis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                                                                  standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTC----CGTACACTTTTTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACATCCAGATGACCCAGTCTCCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrProProIleThrPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyLysAlaProLysLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAlaArgCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    viruses,
                                                                                                                                                                                                                                                                                      (first entry)
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                                                  /label= signal_peptide
23..237
/label= IGFAM-13
38..112
/label= Ig_domain
150..219
/label= Ig_domain
                                                                                                                                  Location/Qualifiers
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606.50
91.97%
88.32%
79.70%
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                    disorder; cancer;
allergy.
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420

102 312 82 252 62 192

132

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the human immunoglobulin superfamily protein IGFAM-13. Its gene was isolated from a cDNA library of lung tumour tissue. It is expressed in reproductive, gastrointestinal and cardiovascular tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable; disgrowing and treating many disease, including cancer, immune system disorders (such as inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, systemic lupus crythematosus and ulcerative colitis), complications of ancer, haemodialysis and extracorporeal circulation, trauma and haematopoietic cancer (such as leukaemia) and infections caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-NOV-1998;
22-DEC-1998;
07-APR-1999;
                                                                                                                                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                                                 193
                    253
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                                                                                                                                                                                                                                                                                                                             Scores:
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DB; AAA27393.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Page 87-88; 105pp;
                                                                                                                                                                                    w
AGGTTCAGCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT
                                   MetThrCysArgAlaSerGinSerIleSerThrTyrLeuAsnTrpTyrGinGlnLysbro
                                              GGTAAAGCACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGTGTCCCATCA
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Lal
                                                                                                      ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA
                                                                                                                                           GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC
                                                                                                                                                                           INCYTE
                                                                                                                             AspileGinMetThrGinSerProSerSerLeuSerAlaSerValGlyAspArgValThr
                                                                                                                                                                                                                                                                                                                                                                        viruses,
                                                                                                                                                                                                                                                                                                                                                 237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P,
                                                                                                                                                                                                                            (1-420) x AAY96301 (1-237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHARM INC.
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Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193..236
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                                                                                                                                                                                                                                                     2.13e-56
606.50
93.43%
86.86%
79.70%
                                                                                                                                                                                                                                                                                                                                                                     fungi or parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
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Yang J;
                                                                                                                                                                                                                                                               Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                    Gaps:
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Matches:
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             312
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The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also CC encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to CC recombinant vectors and host cells comprising human ovarian antigen CC polynucleotides, antibodies against human ovarian antigens, and the use CC of ovarian antigen polynucleotides and polypeptides in diagnosing, CC treating, prognosing or preventing various ovary and/or breast-related CC metastatic tumours of ovarian or breast origin, reproductive system CC disorders (e.g., infertility, disorders of pregnancy, anovulation, CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine CC disorders, infections (e.g., chamydia, HIV, toxoplasmosis, and toxic cyginitis), immune disorders (e.g., congenital and acquired communodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), conditions (e.g., anaemia), cardiovascular disorders, include on the conditions (e.g., anaemia), cardiovascular disorders, include on the conditions (e.g., anaemia), cardiovascular disorders, include on the conditions (e.g., anaemia), cardiovascular disorders, include on the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID No 4289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndror POOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ovarian antigen HVVCI50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP43157;
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DB; ABQ56234.
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neurological diso
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                           Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; cardiovascular disorder; respiratory disorder; neurological disorder;
            gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; chromosome 2p12.
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:

Conservative: Mismatches: Indels:

US-08-728-463B-220 (1-420) x ABP41164

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47 73 27

GACATCCAGATGACCCAGTCTCCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAlaArgCys

132 46 72

ATGATGGTCCCAGCTCCAGCTCCTCGGTCTCCTGCTGCTTCCCAGGTTCCCAGATGC

(1-260)

Gaps:

AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr

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cc shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and cryaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), cc immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), cc immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), cc immunodeficiencies (e.g., anaemia), cardiovascular disorders, cc and urinary system disorders. Ovarian antigen polypeptides and cc modulate ovarian antigen expression or activity. The polynucleotides may also be used in socreening for compounds which cc modulate ovarian antigen expression or activity. The polynucleotides may cf further be used for gene therapy, chromosome mapping, in the cidentification of individuals and in forensic analysis, and the cc polypeptides may be used as food additives or to prepare antibodies couseful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention.

Cc Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABC54131-ABC56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing. Treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenornhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome) inflammatory conditions (e.g., satistic conductive and shorters of pregnancy and toxic shock syndrome) inflammatory conditions (e.g., satistic conductive and shorters).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful in the prevention, treatment and diagnosis of cancer (e. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases -
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8.47e-56
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91.18%
86.03%
78.98%
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Matches:
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RESULT 9
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                                              1992-007468/01.
DB; AAQ20067.
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23..234
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                                                                                                                                                                                                                                                                                                                                                           label= Framework_4
28..234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label= CDR_2
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RESULT 10
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                                                                                                Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis; Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy; signal transduction inhibition; tissue fibrosis; atherosclerosis.
                                                                                Homo sapiens.
                                                                                                                                                      Human protein SEQ ID
                                                                                                                                                                              22-AUG-2001
                                                                                                                                                                                                        AAB99115;
                                                                                                                                                                                                                             AAB99115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The variable region of the light chain is used in a recombinant protein with the variable region from the heavy chain of 3D6, the two V regions being joined by a linker. The recombinant protein binds to HIV 9p160. See also AAQ20066 and AAQ20068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV-1 - contains variable region of antibody derived from 3D6 cell line, used for detecting HIV-1 antigen _{\mbox{\scriptsize 0}}
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599.00
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17-NOV-2000; 2000WO-JP08129.

25-MAY-2001 WO200136642-A1

Monoclonal antibody; MAb; RF-1; RF-2; respiratory syncytial virus; RSV; fusion protein; F-protein; vaccine; immunotherapy; therapy;

virus; immortalisation; recombinant antibody.

Epstein

Human

anti-RSV monoclonal antibody RF-1 light

chain.

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RESULT 11
AAW11638
ID AAW11
XX
AC AAW11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel human monoclonal antibodies. The antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II receptor, resulting in the inhibition of the signal transduction of human TGF-beta into cells. The antibodies can be used for the prevention and treatment of diseases associated with the production of TGF-beta, such as tissue fibrosis in the lung, liver, skin, kidney or other tissues, atherosclerosis, atopy, keloid and arthritis. The present sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful
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08-NOV-2000; 2000JP-0340216.
            13-MAY-1997
                                                AAW11638
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                 standard;
                                                                                     GlyThrLysValGluIleLysArgThrValAlaAlaProSerValPhe
                                                                                                        GGAACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTTC
                                                                                                                         GluAspPheAlaThrTyrTyrCysLeuGlnHisAsnSerAsnProLeuThrPheGlyGly
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           (first entry)
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597.00
90.44%
86.76%
78.45%
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                                                Protein;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                              Alignment Scores: Pred. No.:
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A polypeptide (AAW11638) comprises a leader sequence, RF-1 light chain variable region (see also AAW11634), and human kappa constant region. RF1 is a human monoclonal antibody. (hMAb) specific for the fusion protein of respiratory syncytial virus (RSV). The polypeptide can be produced in eukaryotic host (e.g. CHO) cells transfected with vector NEOSPLA incorporating a DNA construct (AAT61240) including the RF-1 VL sequence. The and RF-2 heavy and light chains (see also AAW11639-41) are similarly produced. The transfected host cells provide a constant, stable supply of anti-RSV F-protein hMAbs for use in the treatment or prevention of RSV infection.
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Peptide
                                                                                                                                                                                                                                                                                       Human monoclonal antibody specific for respiratory syncytial virus fusion protein - used for the prevention and treatment of RSV
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N-PSDB; AAT61240.
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Sequence
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/note= "framework region
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|18..127
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ion; inflammation; haematopoiesis; AIDS; allergy.
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98US-0113635.
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38..112
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The present sequence is the human immunoglobulin superfamily protein IGPAM-9. Its gene was isolated from a cDNA library of breast tumour tissue. It is expressed in reproductive, gastrointestinal and immune and anematopoletic tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for disgnosing and treating many diseases, including cancer, immune system at arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative colitis, complications of cancer, haemodialysis and extracorporeal circulation, trauma and cancer (such as leukaemia) and infections caused by
                                                                                                                                                                                                                                                                                                                                      Immunoglobulin superfamily proteins, the agonist and antagonist of th protein is useful for preventing and treating disorders associated wi altered levels of the protein such as cancer, immune system disorders
                                                                                                                                                                                                                                                                                             Claim 1;
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                        viruses, fungi or parasites.
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Hillman
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                                            GluAspPheAlaThrTyrTyrCysGlnGlnHisHisSerTyrProLeuThrPheGlyGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotides encoding the L and H chains of human anti-HBs Ab are given in AAQ49943-Q49944. The Ab can be easily produced large quantities for therapeutic use.
                                                                                                                             Monoclonal
                                                                                                                                         Anti-interleukin-1-alpha human monoclonal antibody VL segment
                                                                                                                                                       04-NOV-1995
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                                                                                                                    antiinflammatory;
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                                                                                                                                                                                  standard;
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                                                                                                                    antibody; interleukin-1-alpha;
matory; prophylactic; therapeut;
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81.62%
76.87%
                                                                                                                                                                                  Protein;
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                                               "CDR 1 (+24
                                                             "Framework (FR) 1 (+1
                                                                           "signal
                    "CDR 2
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                                  (+35
        (+57
                    (+50 to +56)"
                                                                           peptide"
                                                                                                                   n-1-alpha; cytokine;
therapeutic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human monoclonal antibody against medicament to treat inflammation.
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DB; AAQ87237.
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               GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAG
                                                              MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpPheProGlySerArgCys
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GluAspPheAlaThrTyrTyrCysGlnGlnThrSerSerPheLeuLeuSerPheGlyGly
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by the cDNA isolated as clone 1666486 from the Incyte BMARNOTO3 library. The human IMOLB (AAB15336-B15550) and their encoding polynucleotides (AAA95775-A95789), and compositions comprising them are useful for the control of infections and cell proliferative disorders, including cancer. The IMOL may be used to treat or prevent disorders, including cancer. The IMOL cexpression or activity of IMOL, such as immunological disorders. CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease), coronavirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus, Streptococcus, Irreptococcus, Irreptococcus, CC Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g. CC glasmodium, Trypanosoma, intestinal protozoa), cell proliferative cuseful as immunogens for the development of antibodies that specifically recognizes these peptides. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which compounds in drug screening techniques. Antibodies which specifically compounds in drug screening techniques. Antibodies which specifically be used for the disease, as targets in a carrier and affected individuals, and for screening libraries of by expression of IMOL may be used for the disgnosis of disorders characterized by expression of IMOL, or in assays to monitor patients being treated XX with IMOL or agonists, antagonists, or inhibitors of two-
                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                       No.:
                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human immune system molecules 1-15 and polynucleotides encoding them useful for diagnosing, treating or preventing e.g. immunological disorders, infections, cell proliferative disorders, microbial
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N-PSDB; AAA95785.
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05-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarteriosclerotic; antiasthmatic; antidiabetic; nephrotropic
antigout; dermatological; antithyroid; virucide; hepatotropic;
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       Disclosure;
                    Human anti-hepatitis B surface antigen antibody gene - outlined to produce L and H chains of the antibody in large
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123 GlyThrLysValGluHisLysArg 130

Search completed: June 3, 2003, 09:02:30 Job time: 29.3328 secs

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Command line parameters:

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-Q-/cgn2 1/USPTO_spool/US08728463/runat_03062003_085618_16959/app_query.fasta_1.3690
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Copyright (c) 1993 - 2003 Compugen Ltd
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ALIGNMENTS

Sequence 30, Application US/09859053 Patent No. US20020102658A1

GENERAL

INFORMATION:

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Alignment Scores: Pred. No.:
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APPLICANT: Tsuji, Takashi
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658Aluaki
APPLICANT: HORI, WONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                                                   SOFTWARE: FastSEQ
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                                                                                                    LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
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     3.82e-49
Length:
     236
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GENERAL INFORMATION:

APPLICANT: BRAMS, PETER

APPLICANT: MORROW, PHILLIP

ITILE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES

TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES

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TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES

TITLE OF INVENTION: NEUTRALIZING THERAPEUTIC USE THEREOF

FILE REFERENCE: 037003-0275759

CURRENT APPLICATION NUMBER: US/09/740,002

FURRENT APPLICATION NUMBER: 09/335,697

PRIOR APPLICATION NUMBER: 09/335,697

PRIOR APPLICATION NUMBER: 09/335,697

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SOFTWARE: PatentIn version 3.1
SEQ ID NO 69
LENGTH: 236
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
                                                                                                                                                                                                                             US-08-728-463B-220 (1-420) x US-10-006-593-69 (1-236)
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                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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CURRENT FILING DATE: 2001-12-05
FRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
NUMBER: US 60/294,068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bowdish, Katherine S. APPLICANT: Frederickson, Shana APPLICANT: Renshaw, Mark
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TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
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ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 192
                                          AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr
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Wo. US20030049683A1
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-740-002-26
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 26
LENGTH: 234
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APPLICANT: MORROW, PHILLIP
APPLICANT: MORROW, PHILLIP
ITTLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1995-06-07
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Conservative:
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Best Local Similarity:
Query Match:
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LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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GENERAL INFORMATION:
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APPLICANT: Athwal, Dilject Singh
APPLICANT: Emtage, John Spencer
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
FILE REFERENCE: CARP-0088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/855,271
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/347,061
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
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US20020042089A1
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|GlyThrLysValGluValLysArg 128
                                 GGAACCAAGCTGGAGATCAAACGA 396
                                                                                GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAG
                                                                                                                              GlyLysAlaProLysLeuLeuIleTyrGlyAlaAsnSerLeuGlnThrGlyValProSer
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RESULT 7
US-10-153-382-19
US-10-153-382-19; Sequence 19, Application US/10153382; Publication No. US20030086930A1; GENERAL INFORMATION:
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; NAME/KEY: SITE
; LOCATION: (120)
; OTHER INFORMATION: X
US-09-800-729-150
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Best Local Similarity:
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PRIOR APPLICATION NUMBER: PCT/U
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/15;
PRIOR FILING DATE: 199-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Var
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 150
LENGTH: 234
                                                   APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE RÉFERENCE: PC23019A
                      CURRENT FILING DATE: 2002-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Patent No. US20020068319A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: PZ044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
FILE REFERENCE: PZO
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        APPLICATION NUMBER:
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                                                                                                                                                                                                                   GGAACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTTC 420
                                                                                                                                                                                                                                                                   AspAspValAlaThrTyrSerCysGlnGlnTyrAsnThrPheProLeuThrPheGly***
                                                                                                                                                                                                                                                                                                 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAG 372
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74.26%
70.17%
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                   Score:
                                                                                 Pred.
                                                                                             Alignment Scores:
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US-09-798-058-4
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                                                                                                                                                             SEQ ID NO 4
LENGTH: 109
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09798058 Patent No. US20020098523A1
                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/187,246 PRIOR FILING DATE: 2000-03-03 NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Human antibodies against eotaxin and their FILE REFERENCE: 84632-000100 CURRENT APPLICATION NUMBER: US/09/798,058 CURRENT FILING DATE: 2001-08-29
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Vaughan, Tristan Joh
APPLICANT: Wilton, Alison Jane
APPLICANT: Smith, Stephen
APPLICANT: Main, Sarah Helen
                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                               ORGANISM: Homo sapiens
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Tristan John

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6.67e-38 526.50 97.25% 95.41% 69.19%

Length: Matches:

Indels: Gaps:

Mismatches: Conservative:

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; PRIOR FILING DATE: 2001-05-23; NUMBER OF SEQ ID NOS: 39; SOFTWARE: PatentIn Ver. 2.1; SEQ ID NO 19; LENGTH: 214; TYPE: PRT; ORGANISM: Homo sapiens
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Pred. No.:
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GAAGATTTTGCAACTAACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTTGGTCAG
                                                                           GluAspPheAlaThrTyrTyrCysGlnGlnTyrTyrSerThrProPheThrPheGlyPro
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529.00
93.97%
89.66%
69.51%
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Matches:
Conservative:
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RESULT 9
US-10-283-349-71
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Publication No. US2003
GENERAL INFORMATION:
                     TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 71:
                                                                                                                                                                       APPLICATION NUMBER: JP 232384/95 FILING DATE: 11-SEP-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HANAI, No. US20030096977Aluo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0
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                                                                                                                NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/283,349 FILING DATE: 29-Oct-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1155, A:
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluAspPheAlaThrTyrTyrCysGlnGlnAlaSerSerPheProSerIleThrPheGly
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     CHARACTERISTICS:
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IIDA, Akihiro
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 Best Local Similarity:
Query Match:
                                       Percent Similarity:
                                                                                                Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-800-729-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
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                                                                                                                                   US-09-800-729-152
                                                                                                                                                                                                                                                             TITLE OF INVENTION: 32 Human secreted prote FILE REFERENCE: PZ044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-2
PRIOR FILING DATE: 1000-09-2
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
                                                                                                                                                     ; SEQ ID NO 152
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo s
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 152, Application US/09800729
Patent No. US20020068319A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                            No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 GGAACCAAGCTGGAGATCAAA 393
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121 GlyThrLysValGluIleLys 127
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                          PatentIn Ver.
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85.83%
81.10%
68.86%
1.48e-37
522.50
83.82%
77.21%
68.66%
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                                     Length:
Matches:
Conservative:
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Matches:
       Mismatches:
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Indels:
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   Indels:
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RESULT 11
US-09-940-166A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09940166A Patent No. US20020058324A1 GENERAL INFORMATION:
                                          TELEPHONE: 650/225-7467
TELEPAX: 650/552-981
INFORMATION FOR SEQ ID NO: 2:
$EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/940,166A
FILING DATE: 27-Aug-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 09/097,309
APPLICATION NUMBER: 09/097,309
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTMARE: Windatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                             NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Blank, Gregory S.
Narindray, Daljit S.
Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
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      TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluAspSerAlaThrTyrTyrCysGlnGlnAspTyrThrThrPro---LeuPheGlyGln 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
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                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF SEQUENCES:
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Best Local Similarity:
Query Match:
DB:
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US-09-811-384-11

; Sequence 11, Application US/09811384

; Patent No. US20020081294A1

; GENERAL INFORMATION:
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No.:
             APPLICATION NUMBER: 09/251652
FILING DATE: 17-FEB-2000
APPLICATION NUMBER: 08/788800
FILING DATE: 22-JAN-1997
APPLICATION NUMBER: 60/093038
FILING DATE: 23-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/811,384
FILING DATE: 20-Dec-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                         ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb |

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bednar, Martin M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: South San F
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyThrLysValGluIleLysArgThrValAlaAlaProSerValPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF SEQUENCES: 15
Love,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomas, G. Roger
Gross, Cordell E
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Query Match:
                                                                                              ; OTHER INFORMATION: Synthetic US-10-227-694-1
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 Best Local Similarity:
                  Percent Similarity:
                                                           Alignment Scores:
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                                                                                                                                         SEQ ID NO 1
LENGTH: 237
TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10227694
Publication No. US20030077739A1
GENERAL INFORMATION:
                                                                                                                                                                                                       APPLICANT: Simmons, Laura
APPLICANT: Andersen, Dana
TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND
FILE REFERENCE: P1867R1
CURRENT APPLICATION NUMBER: US/10/227,694
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: US 60/315,209
PRIOR PILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                              FEATURE:
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                                                   No.:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
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TYPE: Amino Acid
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2.45e-37
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                Length:
Matches:
Conservative:
 Mismatches:
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DB:
US-09-940-166A-6
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Patent No. US20020058324A1
GENERAL INFORMATION:
                                                                                                 INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOPETWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/940,166A

FILING DATE: 27-AUG-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION NUMBER: 09/097,309

APPLICATION NUMBER: 09/097,309

APPLICATION NUMBER: 09/097,309

APPLICATION NUMBER: 09/097,309

APPLICATION NUMBER: 09/097,309

APPLICATION NUMBER: 09/097,309
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Narindray, Daljit S.
Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
                                                                                                                                                                  NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
STREET: 1 DNA Way
                    SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 GluAspPheAlaThrTyrTyrCysGlnGlnGlyAsnThrLeuProProThrPheGlyGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: South San
                                                               TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                          TOPOLOGY: Linear
                                                                                 LENGTH: 237 amino acids
                                                                                                                                                TELEFAX: 650/952-9881
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Alignment Scores:

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SOPTWARE: PatentIn Ver. 2
SEQ ID NO 1881
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1881
US-08-728-463B-220 (1-420) x US-09-880-748-1881 (1-244)
                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-880-748-1881
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PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1881, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAG 372
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                                                3.65e-37
518.00
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90.18%
68.07%
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                                          Conservative: Mismatches: Indels: Gaps:
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61 GGTTCCAGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGA 120

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233 ThrPheGlyGlyGlyThrLysValGluIleLysArg 244	361 ACTTTTGGTCAGGGAACCAAGCTGGAGATCAAACGA 396	213 SerLeuGlnProGluAspPheAlaThrTyrTyrCysGlnGlnAlaAsnSerPheProLeu 232	301 AGCCTGCAGCCTGAAGATTTTGCCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTAC 360	193. GlyValProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 212	241 GGTGTCCCATCAAGGTTCAGCGGAAGTGGGATCTGGGACAGATTTCACTCTCACCATCAGC 300	173 GlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSer 192	181 CAGCATAAACCAGGTAAAGCACCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGT 240	153 AspArgValThrIleThrCysArgAlaSerGlnGlyIleSerSerTrpLeuAlaTrpTyr 172	121 GACAGAGTCACCATCACTTGTCGGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTAT 180	

Search completed: June 3, 2003, 09:51:26 Job time: 19.8452 secs

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Command line parameters:

-MODEL-frame+ n2p.model -DEV=xlp
-Q-Ggn2_1/USPTO_spool/US08778463/runat_03062003_085615_16867/app_query.fasta_1.3690
-Q-Ggn2_1/USPTO_spool/US08778463/runat_03062003_085615_16867/app_query.fasta_1.3690
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=ra1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dits -START=1 -RND=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-NODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US08728463 @CGN 1 1 97 @runat_03062003_085615_16867 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 s
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Maximum DB
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length: 2000000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2003 Compus
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            US-08-157-101A-5

US-08-259-372A-14

US-08-468-671-14

US-08-217-918-2

US-08-217-918-2

US-08-470-139-26

US-08-470-139-26

US-08-48-26-16

US-08-812-586-16

US-08-69-147-313

US-08-758-417A-313
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            Sequence 5, Appli
Sequence 14, Appl
Sequence 14, Appl
Sequence 2, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 313, Appli
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Sequence
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US-08-157-101A-5
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                                                                STATE:
               TELEPHONE:
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quence 2, Appl	equence 2,	equence 18, App	ence 2, Appl	equence 78, App	nce 8, Appl	equence 6, Appl	nce 2, Appl	equence 2, Appl	псе 10, Арр	equence 6, Appl	e 40, App	equence 2, Appl	e 2, Appl	equence 2, Appl	e 40	equence 11, App	equence 40, App	equence 185, Ap	nce 185, Ap	nce 39,	equence 39,	e 39,	equence 25,	e 25,	equence 25,	equence 25, App	e 71, App	equence 6, Appl	æ	nce 3, Appl	equence 3, Appl

ALIGNMENTS

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APPLICANT: AKIMA, KENJI

APPLICANT: NISHIHARA, TATSURO
TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
TITLE OF INVENTION: PLASMIDS THEREFOR
NUMBER OF SEQUENCES: 9

CORRESPONDENCE : 9
                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PLOSE #1.0, Version #1.25
CURRENT APPLICATION DATA: 05-DR-194
FILLING DATE: 05-DR-1994
CLASSIFICATION: 530
CLASSIFICATION: 530
                                       REFERENCE/DOCKET NUMBER: 94
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 358
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PILLSBURY, STREET: 1100 NEW YORK CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATSUKURA, SHIGE
TSURUOKA, NOBUO
202-822-0944
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                                                                                                                                                                                                                                                                                                                                                                                                                                         BURY, MADISON & SUTRO
YORK AVENUE, N.W.
                                                                                  35843
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TELEX: 6714627 CUCH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acid

Percent Similarity:
Best Local Similarity:
Query Match:

3.7e-56 585.00 90.44% 81.62% 76.87%

Score:

US-08-157-101A-5

MOLECULE TYPE:

peptide

TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear

Alignment Scores:

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US-08-728-463B-220 (1-420) x US-08-157-101A-5 (1-236)
                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLON
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPA
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DDS/MS-DOS

SOPTWARE: PACENTIN Release #1.0, Ver.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/259,372A

FILING DATE: 14-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTTC 420
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PRODUCTION OF HUMAN MONOCLONAL
ANTIBODIES SPECIFIC FOR HEPATITIS
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Matches:
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Indels:
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RESULT 3
US-08-468-671-14
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Best Local Similarity:
Query Match:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: SMith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1182:
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 326-2400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
IENCTH: 738 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE: 15-JUN-19
PRIOR APPLICATION DATA;
APPLICATION NUMBER: US
FILLING DATE: 11-MAY-19
PRIOR APPLICATION DATA;
APPLICATION NUMBER: US
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APPLICATION NUMBER: US 07
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                             25 ThrGlnSerProSerSerValSerAlaSerValGlyAspArgValThrValThrCysArg
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                                               AspPheLysArg
                                                                                                                                        ACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAGGGAACCAAGCTG 384
                                                                                                                                                                                    SerGlySerGlyThrAspPheThrLeuThrIleThrSerLeuGlnAlaGluAspPheAla
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                                                                                                                ThrTyrTyrCysGlnGlnAlaAspSerLeuProPheThrPheGlyGlyGlyThrLysVal
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94.35%
88.71%
75.95%
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                                                                                                                  124
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RESULT 2 US-08-259-372A-14 ; Sequence 14, Applic ; Patent No. 5565354

123 373 103

CLASSIF#CATION:

14-JUN-1994 N: 424

CITY: San Francisco STATE: CA

COUNTRY:

USA

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RESULT 5
US-08-812-586-45
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                 Alignment Scores: Pred. No.:
                                                                  US-08-812-586-45
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Patent No. 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                    TELEFAX: (212) 391-0525 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,586
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400 TELEFAX: (212) 391-0525
                                                                                                   STRANDEDNESS:
TOPOLOGY: 1i
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                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036
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1185 Avenue of the Americas
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PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYM (AAA)
DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
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                 Length:
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DB:
                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
                              US-08-728-463B-220 (1-420) x US-08-470-139-26 (1-128)
                                                                                                                                 Score:
                                                                                                                                                Pred. No.:
                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                  US-08-470-139-26
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Patent No. 5998586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: TRUJILLO, DOREEN YATKO
REGISTRATION NUMBER: 35,719
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 06 JUNE-1
CLASSIFICATION: 536
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NUMBER OF SEQUENCES: 20
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                  TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379
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13 ATGATGGTCCCAGCTCAGCTCCTCGGTCTCCTGCTGCTCCTGGTTCCCAGGTTCCAGATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTGCAACTTACTATTGTCAACAGGCTAATAGTTTTCCCGTACACTTTTTGGTCAGGGAACC 378
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N: 536
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Matches:
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Best Local Similarity:
                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                       JS-08-468-671-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 128 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 06/90 FILING DATE: 05-SEP-1986 ATTORNEY/AGENT INFORMATION: NAME: Smith, William M. REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/468,671 FILING DATE: 06-UN-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 31-OCT-1986 PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "
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                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0' FILING DATE: 27-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 51-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/192,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO.
85 ACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCGG 144
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5648077
                                                                       GCTCAGCTCCTCGGTCTCCTGCTCCTGGTTCCCAGGTTCCAGATGCGACATCCAGATG
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US-08-728-463B-220 (1-420) x US-08-217-918-2 (1-129)
                                                            Percent Similarity:
Best Local Similarity:
                                                                                                    score:
                                                                                                                    Pred. No.:
                                                                                                                                  Alignment Scores:
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                                                                                                                                                                     US-08-217-918-2
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
AMME: Smith, Willaim M
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08217918
Patent No. 5506132
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,918
FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LAKE, PHILIP
APPLICANT: OSTBERG, LARS
TITLE OF INVENTION: HUMAN ANTIBODIES
TITLE OF INVENTION: VARICELLA-ZOSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Townsend and Townsend Khourie and
                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                                    TYPE: am:
TOPOLOGY:
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Matches:
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                                                   US-08-728-463B-220 (1-420) x US-08-569-147-80 (1-128)
                                                                                                     Query Match:
                                                                                                                     Best Local Similarity:
                                                                                                                                      Percent Similarity:
                                                                                                                                                         Score:
                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                        ; MOLECULE TYPE: US-08-569-147-80
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HU
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0047
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/569,147
FILING DATE: 25-March-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
BROTETBATTON NUMBER: 25 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 6180377ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                            LENGTH:
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13 ATGATGGTCCCAGCTCCAGCTCCCTCCTGCTCCTGGTTCCCAGGTTCCAGATGC
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                                                                                                                                                                                                                                                                                            128 amino acids
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                                                                                                                                                                                                                                                                                                                                                                 (215) 568-3100
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88.28%
81.25%
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                                                                                                    Mismatches: Indels:
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RESULT 10
US-09-042-353-48
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                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Anima
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                               FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
                                                                                         FILING DATE: 26-APR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 16-DE
                                                                                                                                                                                                                          APPLICATION NUMBER: US 0'
FILING DATE: 23-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1:
CLASSIFICATION:
                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                   APPLICATION NUMBER
                                                                         APPLICATION NUMBER:
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                                                                                                                                                                     UMBER: US 07/990,860
16-DEC-1992
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18-NOV-1993
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                 US 08/155,301
                                                                         US 08/096,762
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; PEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: No. 6316227el Sequence
US-09-347-061-26
                                                                                                                                                                                                                                                            US-08-728-463B-220 (1-420) x US-09-347-061-26 (1-128)
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Best Local Similarity:
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SEQ ID NO 26
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Patent No. 631622
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CURRENT APPLICATION NUMBER: US/09/347,061
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: DATC: 28
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APPLICANT: Athwal, Dilject Singh
APPLICANT: Emtage, John Spencer
TITLE OF INVENTION: Interleukin
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                                                 IleThrCysLeuAlaSerGluGlyIleSerSerTyrLeuAlaTrpTyrGlnGlnLysPro
                                                                      ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA
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                                                                                                                                    US-08-728-463B-220 (1-420) x US-08-812-586-16 (1-235)
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Best Local Similarity:
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US-08-812-586-16
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ. ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
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FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
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                                                               AlaIleArgIleAlaGlnSerProSerSerLeuSerAlaSerThrGlyAspArgValThr
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                                                                                                                                                                                                                                                                                                                                                                                           235 amino acids
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1185 Avenue of the Americas
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VENTION: PURIFIED AND RECOMBINANT ANTIGENIC
VENTION: PURIFIED AND RECOMBINANT ANTIGENIC
VENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
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Matches:
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US-08-728-463B-220 (1-420) x US-09-042-353-48 (1-117)
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
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313 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCG 357
                                                                                                           63 GluLysAlaProLysSerLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 82
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                                                                                                                                                                                                                                                                                                                                     MetArgValLeuAlaGlnLeuLeuGlyLeuLeuLeuCeuCysPheProGlyAlaArgCys
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                                                                      AGGTTCAGCGGAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 312
                                                                                                                                                                                                                                                              AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr
                                     ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro
                                                                                                                                                                                      IleThrCysArgAlaSerGlnGlyIleSerSerTrpLeuAlaTrpTyrGlnGlnLysPro
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09-MAR-1994
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01-DEC-1997
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RESULT 11
US-08-758-417A-313
                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID

US-08-758-417A-313
Query Match:
DB:
                              Percent Similarity:
Best Local Similarity:
                                                                               Alignment Scores: Pred. No.:
                                                                 Score:
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Patent No. 6300129
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                             NAME: Serafini,
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/990,860 FILING DATE: 16-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
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                                                                                                                                                                                                            LENGTH: 117 amino acids
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APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/096,762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PELICATION NUMBER: US 08/352,322
ILING DATE: 07-DEC-1994
PELICATION NUMBER: US 08/209,741
ILING DATE: 09-MAR-1994
PELICATION NUMBER: US 08/165,699
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Matches:
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Alignment Scores:
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US-07-934-373C-3
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                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy diversely for compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentéch)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/934,373C

FILING DATE: 21-Aug-1992

CLASSIFICATION DATA:

APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:
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                                                                                                                                     TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/7
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Faul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
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                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                        NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                                                                                                      LENGTH:
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                                                                           Linear
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Best Local Similarity:
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                                                                         CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/93437
FILING DATE: 21-AUG-1992
PRIOR APPLICATION UNMBER: 08/
PRILING DATE: 17-NOV-19
PRILING DATE: 17-NOV-19
PRICH APPLICATION DATA: 17/US92/05126
APPLICATION NUMBER: 1/992
FILING DATE: 15-UK
PRIOR APPLICATION DATA: 15-UK
PRIOR APPLICATION DATA: 17/N15272
APPLICATION NUMBER: 1/991
FILING DATE: 17-WTON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5 inch, 1.44 Mb;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                  ATTORNEY/AGENT TORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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NAME: Lee, Lindy M. 40,378 REGISTRATIO NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 09-May
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1 DNA Way
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A;Reference number: S23716; MUID:92031262; PMID:1718404 A;Reference number: S23717
A;Molecule type: mRNA
A;Residues: 15-111 <HAW>
A;Cross-references: EMBL:X54441
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>F;5-140/Product: Ig heavy chain (fragment) #status predicted <MA1
F;29-111/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-140 <4AR>
A;Residues: 1-140 <4AR>
A;Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder
Int. Immunol. 3, 865-875, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Harindranath, N.
submitted to the EMBL Data
A;Reference number: S78051
A;Accession: S78052
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Date: 19-Nov-1997 #sequence_revision
Accession: $78052; $23717
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                TGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTACAACCCGTCCCTCAAGAGTCGA
                                                                              GGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGTAAGGGGCTGGAG
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TrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArg
                                                              GlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGlu
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A;Title: Somatic diversification in the heavy chain variable A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37782
A;Status: preliminary
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig variable region (VDJ) (clone T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: I37782; S25476
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C;Species: Homo sapiens (man)
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A; Residues: 1-140 < RES>
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                                                                         SerTrpTyrGlyArgTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer
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-Q=/cgm2_1/USPTO_spool/US08728463/runat_03062003_085615_16827/app_query.fasta_1.3690
-Q=/cgm2_1/USPTO_spool/US08728463/runat_03062003_085615_16827/app_query.fasta_1.3690
-DB=PIR_73_-QFMT=fastan_-SUFFIX=rpr_-MINATCH=0.1_-LOOPGL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MX==100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=2000000000
-USER=US08728463_@CGN_1_1_177_@runat_03062003_085615_16827_-NCPU=6 -ICPU=3
-NO_MMAP_-LARGEQUERY_NEG_SCORES=0 -WAIT-DSPBLOCK=100 -LONGLOG
-DEV_TIMEQUT=30 -THREDUT=30 -THREDS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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A;Cross-references: GB:S39381; NID:g250899; PIDN:AAB22441.1; PID:g250900
A;Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBIP:108089)
C;Superfamily: immunoglobulin Vegion; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>
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A;Title: An antile 11 autoantibody from Wiskott-Aldrich syndrome which recognizes i b A;Reference number: A49045; MUID:92324290; PMID:1623923
A;Accession: A49045
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                       GTGCAGCTACAGCAGTGGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACC
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A;KCCESSACH.
A;KOTATUS: preliminary
A;Molecule type: mRNA
A;Rosidues: 1-139 <CUI>
A;Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979
A;Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979
C;Kuperfamily: immunoglobulin V region; immunoglobulin homology
C;Kupwords: heterotetramer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>
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A;Description: Mechanisms that generate human immunoglobulin diversity operate
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Species: Homo saptens (man)
Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
Accession: S31586
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                                                                                   TCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCCCTGAAG
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R;Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.
Gene 33, 181-189, 1985
A;Title: A cloned human immunoglobulin heavy chain gene
A;Title: A cloned human immunoglobulin heavy chain gene
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A;Map position: 14q32.33-14q32.33
A;Introns: 16/3
C;Superfamily: immunoglobulin V region; immunoglobulin l
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: signal sequence #status predicted <SIG>F;1-19/Domain: signal sequence Training F;20-146/Product: Ig heavy chain V-II region (ARH-77) #F;20-117/Region: V segment
F;35-117/Domain: immunoglobulin homology <IMM>
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C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987
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A; Residues: 1-146 < KUI
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RESULT 5
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Ig heavy chain V region precursor - human
C; Species: Homo sapiens (man)
C; Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: $13519
R; Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A; Title: Immunoglobulin variable heavy chain cDNA sequence from a patient will A; Reference number: $13519
A; Reference number: $13519; MUID:91187691; PMID:2011536
A; Status: preliminary
A; Molecule type: mNNA
A; Residues: 1-47 < MOR>
A; Cross-references: EMBL: X56158; NID:937724; PIDN:CAA39626.1; PID:937725
C; Koywords: heterotetramer; immunoglobulin
C; Koywords: heterotetramer; immunoglobulin homology
C; Molecule type: molecule type: molecule type: MORS
A; Cross-references: EMBL: X56158; NID:937724; PIDN:CAA39626.1; PID:937725
C; Koywords: heterotetramer; immunoglobulin homology
C; Koywords: heterotetramer; immunoglobulin homology
C; Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule type: Molecule ty
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R;Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D submitted to the EMBL Data Library, July 1994
A;Description: The role of the immunoglobulin heavy chain in A;Reference number: S47009
A;Accession: S47010
A;Status: preliminary
A;Molecule type: mRNA.
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-126 <MAH>
A;Residues: 1-126 <MAH>
A;Cross-references: EMBL:Z35492; NID:g517254; PIDN:CAA84625.1; PID:g517255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
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;Species: Homo sapiens (man)
;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-137 <CUI>
A;Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032
A;Cross-references: EMBL:Z14182; NID:g31031; immunoglobulin homology
C;Superfamily: immunoglobulin v region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 10-Nov-
C;Accession: S31676
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; F
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human
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581.50
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Percent Similarity:
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Query Match:
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A;Notecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-139 <CUL)
A;Residues: 1-139 <CUL)
A;Cross-references: EMBL:Z14194; NID:g30975; PIDN:CAA78563.1; PID:g30976
A;Cross-references: EMBL:Z14194; NID:g30975; mmunoglobulin homology
C;Superfamily: immunoglobulin v region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31696
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
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A; Accession: S31696
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 GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTTCGGAGACCCTGTCCCTCACC 120
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                                                              ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
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                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                    C;Keywords: immunoglobulin
F;1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F;18-145/Product: Ig heavy chain (fragment) #status predicted <MA:
F;32-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S23720
A;Molecule type: mRNA
A;Residues: 18-115 < HAW >
A;Cross-references: EMBL:X54445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Harindranath, N.; Goldfarb, I.S.; Iken
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes
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A; Residues: 1-145 < HA
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                                                          CTGAGCTCTGTGACCGCCGCGGACACGCCTGTGTATTACTGTGCGAGA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL:X54445; NID:g37817; PIDN:CAA38312.1; PID:g37818
Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilde:
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82.07%
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RESULT 10
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C;Species: 30
C;Accessic
R;Ratech,
Biochem. E
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A;Status: preliminary
A;Status: preliminary
A;Molecule: type: mRNA
A;Residues: 1-155 <CHA>
A;Residues: 1-155 <CHA>
A;Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; P.C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;47-129/Domain: immunoglobulin homology <IMM>
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(;Species: Homo sagiens (man)
(;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Accession: S31511
G;Accession: S31511
G;Accession: Bemaison, C.; Theze, J.; Zouali, M.
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gen
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              g heavy chain.V-D-J region (RAMOS) - 1;Species: Homo sapiens (man);Date: 30-Jun-1992 #sequence_revision;Accession: PS0341;Ratech, H.
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Matches:
Conservative:
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Indels:
Gaps:
                                          30-Jun-1992
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Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31512
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of an A;Reference number: S31509
A;Reference number: S31509
A;Retatus: preliminary
A;Molecule type: mENA
A;Residues: 1-155 <CHA>
A;Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-133 <RAT'>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                   Alignment
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Best Local Similarity:
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RESULT 14
S09711
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 1:
C;Accession: S09711
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 269, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of A;Reference number: S09710; MUID:90262535; PMID:2111699
A;Accession: S09711
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUGs
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMMs
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Species: Homo sapiens (man)
Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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Keywords: heterotetramer; immunoglobulin
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y Match:
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                                                                              AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCC
                                                                                                                                                                                       CysThrValSerGlyGlySerValSerSerGlyLeuTyrTrpSerTrpIleArgGln
                                                                                                                                                                                                                      TGCGCTGTCTATGGTGGGTCCTTC-----AGTGGTTACTACTGGAGCTGGATCCGCCAG
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                   CTGAAGCTGAGCTCTGTGACCGCCGCGGGGACACGGCTGTGTATTACTGTGCGAGAGTAATT
                                                            СССССАGGTAAGGGGCTGGAGTGGATTGGGGAAATCAATAGTGGAAGCACCAACTAC
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A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG>F;20-116/Product: Ig heavy chain V region 71-4 #status predicteF;34-116/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain precursor V-II region (71-4) - human
(;Species: Homo sapiens (man)
(;Date: 05-Jun-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
(;Accession: B26340
R;Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Hon
J. Mol. Biol. 190, 529-541, 1986
A;Title: Organization and evolution of variable region genes of the human im
A;Reference number: A26340; MUID:87061007; PMID:3097326
A;Accession: B26340
A;Molecule type: DNA
A;Residues: 1-116 <KODD
A;Coss-references: GB:X05711; NID:g33602; PIDN:CAA29183.1; PID:g296660
A;Note: the authors translated the codon GAG for residue 25 as Gln
C;Genetics:
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               CTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGA
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                                                                                        TCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCAAGAACCAGTTCTCTCCCTGAAG
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